

STIC-Biotech/ChemLib

175467

From: Chernyshev, Olga
Sent: Tuesday, January 03, 2006 1:02 PM
To: STIC-Biotech/ChemLib
Subject: 09/869,486; sequence search request

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JAN - 3 2006
STIC-BIOTECH/ChemLib
(STIC)

US case 09/869,486

Please search SEQ ID NO: 25, 29 and 30, and fragment 73-3714 of SEQ ID NO: 29 in regular and pending databases.

Thank you very much!

Olga N. Chernyshev, Ph.D.

AU 1649

REM 3C89

2-0870

mail 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Db 314 TVYDFQEGSEBELDTVLKALVYKCKSHSQEPQYUDELKLAIVAMDRVDIAKSEIFMGDV 373
Qy 419 QMSFHLBLSMDALLNDREPEFVRLISHGLSGHFLTPMRLAQLYSAASNSLIRLTD 478
Db 374 EMBSCDLEBVMVALVSNKPEFVRLFDNGADVADFLTYGLQELVYSVRKSLFLPQLQ 433
Qy 479 QASHSAGTKAPALKGAAELRPP-----DVGHVLEMLGKMKCAPYPSGAWDPH 528
Db 434 RKOBEARLTLAGL--GTQOAREPPAPRPAPSIHEVSRLVDFLODACRGFYQDGRPDGR 491
Qy 529 -----PQGFGEBSMYLLSDKATSPSLDAGLQAPMSDLLMALINRAQMAFYEMWGS 583
Db 492 RAEKGPAPKRPFGQKMLDLNOKS-----ENPMRDLFLMAVLQVRHEMATYFMAMGQ 542
Qy 584 NAVSALGACLLLRVMALEPDAEBAARRKDLAKFEGMGVDFLPGECYSSVRAAALL 643
Db 543 EGVAAALAAKILKEMSHLETBAARAATREA--KYBQLALDLFSECYSSBAAPALLV 600
Qy 644 RRCPELMDATCLOLAMOADAAPFAODGVOSLLTOKMGDMASITPIMAVLAFPCPLI 703
Db 601 RRRRCMSKTCILHATBDKAKAFPAHDGQAFILRIWGMMACTPILRLGAFPCALV 660
Qy 704 YTRLITFRKSEBETREBLE--FDMDSVINGEGVGTADPAKTPLGVPPOSGRPGCCG 761
Db 661 YTNLITF--SEBAPLRTGLBDLQDLSDLTEKSPLYGLQSRVBEVLEAPRAQGD----- 712
Qy 762 RCGGRCC--LRWPHWGAAPVTIFMGVNVSYLLFLILPSRVLLNDQAP--PGSLLEL 816
Db 713 --RGPRAVFLTLTRKRWGAAPVTVFGNVVMPAFLLFTYVLLVDRPPOSGSGEVT 770
Qy 817 LYMAFPLICEBLROGLSGGGSLSAGSGPGRGASLSORLRYLADSMNOCDDVALTCFL 876
Db 771 LYFWVFLVLEIRQGFPTDEBT-----HLVKKFTLYVGDMMKCDVAILFLFI 819
Qy 877 LGVGCRLTPGLYHIGRTVLCIDFVFTVRLLIHIFTVVKOLGPKIVISKMKOVFFFLPF 936
Db 820 VGVTCRMPLSAPFAGRVTLAMDFFVFTLRIIHIFAIHQGLQPKIIVERMKOVFFFLPF 879
Qy 937 LGSVWVAAGVATGELARPDSPPSILRRVTPRYLOIFQOIQEEDMDVALMHSNCSSE 936
Db 880 LSWVLAAYGVTTALMHPDGRLEWIFRRVLYRBYLOIFQOIPLEDEBARV--NCSTH 936
Qy 997 PGFMAPPGAQAGTCVSOYANMLVLLVFLVANIILVNLILAMPSTYFGKVQNSDL 1056
Db 937 PLLLEBSP-----SCBSLYANMLVILLVTLVLTNVLNMLILAMPSTYFOVVOGNADM 991
Qy 1057 YWKAQRYRLIRBPHSAPBALAPPTIVISHRLRLKQLCRPPSPQSSPALBHFVYLSKE 1116
Db 992 FMKFORNYLIVEYHERPALAPPTILSHLSLTLRVPKK-----BAEHKREHLERD 1042
Qy 1117 ----AERKLLTWESYKNEENFLIARADKESDSRLKRTSQVDLAKOIGHIREYQRL 1172
Db 1043 LRPDLQOKVTVWVOENFLSKMEKRRRDSBEGVLEKTAHRVDIFLAKYLGRLBDEKRI 1102
Qy 1173 KVLREYQOCSRVLGVVABALSALLPPGA 1204
Db 1103 KCLBSQINYSVLSVADYLAQ-----GSP 1129

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6874
; LENGTH: 1165
; TYPE: PR
; ORGANISM: Human
US-09-949-016-6874

Query Match 38.4%; Score 2448.5; DB 2; Length 1165;
Best Local Similarity 45.6%; Pred. No. 1.6e-223;
Matches 534; Conservative 177; Mismatches 350; Indels 11; Gaps 26;

Qy 76 GELDFTGAKRHSNPLRLSRTDPAVYSLVTTWGRANLVYSVSGSGGFPYLTQW 135
Db 26 GEVNFQSGGKRRKQFVRVPSGVAHSVLLLEMLPAENLVSVLVBEGQPPAMKSMWR 85
Qy 136 DLRRGLVRAAGSTGAMIVTGLHTGIGRHVAVVRDHOMASTG-GTKVAMGVAPWGVV 194
Db 86 DVLRKGLVKAAGSTGAMILTSALRVGLARVGOAVRDHSLASTIKRVVAVGMAISGRV 145
Qy 195 RNRDTLINPKSGSPARYRWGDEPD--GVQFP--IDYNSAFELYDDGTHGCLGENRF 249
Db 146 LHRRIIEBAQEDFPVHY-----PEDDQSGGFCISDSNLSHFLVPEGPBGKDGTL 200
Qy 250 RLRLSEYISQOKTGVGTG-IDIPVLLILIDGBEKULTRLENNATQOALPCLLVAGSGGA 308
Db 201 RLRLKRIISQAPAGYGGTGISRIPLVCLVMDPNTLERSRVEQALPWLILVSGGIA 260
Qy 309 DCLAETLED--TLAPSGAGQGBARDRIKPPPK-----GDLEVLAQVERIMTRKEL 361
Db 261 DVLAALVNOPHLVP-----KVAEKQFKEKPSKHSFEDVTRTKYLQNTSHQHL 313
Qy 362 TVYSSE-DGSEPEFETVLKALVYAC--GSSKASAYLDELRLAAMNRVDIAQSELFRDI 418
Db 314 TVYDFQEGSEBELDTVLKALVYKCKSHSQEPQYUDELKLAIVAMDRVDIAKSEIFMGDV 373
Qy 419 QMSFHLBLSMDALLNDREPEFVRLISHGLSGHFLTPMRLAQLYSAASNSLIRLTD 478
Db 374 EMBSCDLEBVMVALVSNKPEFVRLFDNGADVADFLTYGLQELVYSVRKSLFLPQLQ 433
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Qy 529 -----PQGFGEBSMYLLSDKATSPSLDAGLQAPMSDLLMALINRAQMAFYEMWGS 583
Db 492 RAEKGPAPKRPFGQKMLDLNOKS-----ENPMRDLFLMAVLQVRHEMATYFMAMGQ 542
Qy 584 NAVSALGACLLLRVMALEPDAEBAARRKDLAKFEGMGVDFLPGECYSSVRAAALL 643
Db 543 EGVAAALAAKILKEMSHLETBAARAATREA--KYBQLALDLFSECYSSBAAPALLV 600
Qy 644 RRCPELMDATCLOLAMOADAAPFAODGVOSLLTOKMGDMASITPIMAVLAFPCPLI 703
Db 601 RRRRCMSKTCILHATBDKAKAFPAHDGQAFILRIWGMMACTPILRLGAFPCALV 660
Qy 704 YTRLITFRKSEBETREBLE--FDMDSVINGEGVGTADPAKTPLGVPPOSGRPGCCG 761
Db 661 YTNLITF--SEBAPLRTGLBDLQDLSDLTEKSPLYGLQSRVBEVLEAPRAQGD----- 712
Qy 762 RCGGRCC--LRWPHWGAAPVTIFMGVNVSYLLFLILPSRVLLNDQAP--PGSLLEL 816
Db 713 --RGPRAVFLTLTRKRWGAAPVTVFGNVVMPAFLLFTYVLLVDRPPOSGSGEVT 770
Qy 817 LYMAFPLICEBLROGLSGGGSLSAGSGPGRGASLSORLRYLADSMNOCDDVALTCFL 876
Db 771 LYFWVFLVLEIRQGFPTDEBT-----HLVKKFTLYVGDMMKCDVAILFLFI 819
Qy 877 LGVGCRLTPGLYHIGRTVLCIDFVFTVRLLIHIFTVVKOLGPKIVISKMKOVFFFLPF 936

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 08:55:56 ; Search time 46 Seconds
(without alignments)
2181.919 Million cell updates/sec

Title: US-09-869-486B-30
Perfect score: 6383
Sequence: 1 MWPBKEQSWIPKIFKKTCT.....RSALLPGGPPPDLPESKD 1214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 8265679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/1aa/5_COMB.pep.*
- 2: /cgm2_6/ptodata/1/1aa/6_COMB.pep.*
- 3: /cgm2_6/ptodata/1/1aa/H_COMB.pep.*
- 4: /cgm2_6/ptodata/1/1aa/PTCUS_COMB.pep.*
- 5: /cgm2_6/ptodata/1/1aa/RB_COMB.pep.*
- 6: /cgm2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2452.5	38.4	1165	2 US-09-949-016-11392	Sequence 11392, A
2	2448.5	38.4	1165	2 US-09-949-016-6874	Sequence 6874, A
3	1945	30.5	1503	2 US-09-600-087-2	Sequence 2, Appl1
4	1945	30.5	1503	2 US-09-949-016-6341	Sequence 6341, A
5	1941	30.4	1529	2 US-09-949-016-11100	Sequence 11100, A
6	1636	25.6	315	2 US-09-020-956-112	Sequence 112, App
7	1636	25.6	315	2 US-09-030-607-112	Sequence 112, App
8	1636	25.6	315	2 US-09-439-313-112	Sequence 112, App
9	1636	25.6	315	2 US-09-352-616A-112	Sequence 112, App
10	1636	25.6	315	2 US-09-232-149A-112	Sequence 112, App
11	1636	25.6	315	2 US-09-159-812-112	Sequence 112, App
12	1636	25.6	315	2 US-09-636-215-112	Sequence 112, App
13	1636	25.6	315	2 US-09-685-166A-112	Sequence 112, App
14	1636	25.6	315	2 US-09-115-453-112	Sequence 112, App
15	1636	25.6	315	2 US-09-688-489-112	Sequence 112, App
16	1636	25.6	315	2 US-09-679-426-112	Sequence 112, App
17	1636	25.6	315	2 US-09-759-143-112	Sequence 112, App
18	1636	25.6	315	2 US-09-651-236-112	Sequence 112, App
19	1636	25.6	315	2 US-09-030-606-112	Sequence 112, App
20	1636	25.6	315	2 US-09-657-279-112	Sequence 112, App
21	1636	25.6	315	2 US-10-012-096-15	Sequence 15, Appl1
22	1606.5	25.2	1095	2 US-09-636-215-778	Sequence 778, App
23	1606.5	25.2	1095	2 US-09-685-166A-778	Sequence 778, App
24	1606.5	25.2	1095	2 US-09-679-426-778	Sequence 778, App
25	1606.5	25.2	1095	2 US-09-759-143-778	Sequence 778, App
26	1606.5	25.2	1095	2 US-09-651-236-778	Sequence 778, App
27	1606.5	25.2	1095	2 US-09-657-279-778	Sequence 778, App

28	1606.5	25.2	1095	2 US-09-657-479-778	Sequence 778, App
29	1606.5	25.2	1095	2 US-10-012-896-778	Sequence 778, App
30	1599.5	25.1	1095	2 US-09-636-215-780	Sequence 780, App
31	1599.5	25.1	1095	2 US-09-685-166A-780	Sequence 780, App
32	1599.5	25.1	1095	2 US-09-679-426-780	Sequence 780, App
33	1599.5	25.1	1095	2 US-09-759-143-780	Sequence 780, App
34	1599.5	25.1	1095	2 US-09-651-236-780	Sequence 780, App
35	1599.5	25.1	1095	2 US-09-657-279-780	Sequence 780, App
36	1599.5	25.1	1095	2 US-10-012-896-780	Sequence 780, App
37	1278	20.0	1533	1 US-08-623-679-9	Sequence 9, Appl1
38	1278	20.0	1533	2 US-08-933-774-9	Sequence 9, Appl1
39	1278	20.0	1533	2 US-09-181-030-9	Sequence 9, Appl1
40	1278	20.0	1533	2 US-09-534-242-9	Sequence 9, Appl1
41	1278	20.0	1533	2 US-09-454-854-9	Sequence 9, Appl1
42	1278	20.0	1533	2 US-09-164-671-9	Sequence 9, Appl1
43	1278	20.0	1533	2 US-09-182-113-9	Sequence 9, Appl1
44	1278	20.0	1533	2 US-08-862-442-9	Sequence 9, Appl1
45	1172	18.4	1497	1 US-08-623-679-7	Sequence 7, Appl1

ALIGNMENTS

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RESULT 1
US-09-949-016-11392
; Sequence 11392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11392
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11392

Query Match      38.4%; Score 2452.5; DB 2; Length 1165;
Best Local Similarity 45.6%; Pred. No. 6.6e-224;
Matches 535; Conservative 177; Mismatches 349; Indels 111; Gaps 26;

QY 76 GELDTGAGKSHNPLRLSDRTDPAVYSVATRTWGPRAVNLVSLGSGGPIVLTQLQ 135
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 26 GENVFSGSGKKRGKGVAVBSGVAPSVFLDLRLMHLPAVNLVSLVGEQPPRMKSLR 85

QY 136 DLRLKGLVRAAGSTGAMVITVGLHTIGTIGRAVGVAVRDHQAATG-GTKVAVGVAPWGVV 194
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 86 DVLRKGLVKAAGSTGAMVITVGLHTIGTIGRAVGVAVRDHQAATG-GTKVAVGVAPWGVV 145

QY 195 RNRDITLNPKGSPPARRYRWGDEPD--GVQPP--LDYNTSAPFLVDGTHGCLGGENRF 249
   :||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 146 LHRRIIEBAQEDPPVHY-----PEDDQSGGPIGCSLDNSHFTLVBPGRPKDGTTEL 200

QY 250 RLRLSIVISOOKTVGGTG-IDIPVLLLLIDGBKMLTRIENTAQLPCLLVAGSGGAA 308
   ||||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 201 RLRLKRIISORAGVGGTGTETIPVCLLVGDBNTLERSRAVEQAAPWLLILGSGGIA 260

QY 309 DCLAEITLED--TLAPSGGARGOGBARDRIIRFPK-----GDLEVTQAQVERITRREL 361
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 261 DVLAALVNOGHLV-----KVAEKQFKEKFPKSKFMSWDIVRTKTLQNTISHQHL 313

QY 362 TVTSSR-DGSEBEPETIVLKLVTAC--GSSEBAGAYLDLRLAVAMNRVVDIAQSELFRGDI 418

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: January 6, 2006, 08:55:52 ; Search time 171 Seconds

(without alignments)
5008.838 Million cell updates/sec

Title: US-09-869-486b-30

Sequence: 1 MVVPEKRGSWIPKIPKKTCTC.....RSALPPGGPPPDLPGRKD 1214

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_09_80.*
2: uniprot_sprot.*
3: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6383	100.0	1214	2	Q8TD43_HUMAN
2	5505.5	86.3	1069	2	Q7Z5D9_HUMAN
3	5454	85.4	1040	2	Q96184_HUMAN
4	5316	83.3	1016	2	Q9NXY1_HUMAN
5	5194.5	81.4	1213	2	Q7TN37_MOUSE
6	4001.5	62.7	945	2	Q8BLM7_MOUSE
7	3564	55.8	872	2	Q6PDM0_MOUSE
8	3375	52.9	686	2	Q8HXH2_MACRA
9	3189	50.0	793	2	Q80194_MOUSE
10	2452.5	38.4	1165	2	Q521U2_HUMAN
11	2448.5	38.4	1165	2	Q9NZ08_HUMAN
12	2437.5	38.2	1159	2	Q9NY34_HUMAN
13	2397.5	37.6	1158	2	Q9BPM4_MOUSE
14	2397.5	37.6	1158	2	Q91JH7_MOUSE
15	2396.5	37.5	1148	2	Q9NRP9_MOUSE
16	2376.5	37.2	1116	2	Q9BPM3_MOUSE
17	2310.5	36.2	1297	2	Q4RYV8_TRYNG
18	2088	32.7	1030	2	Q8B644_MOUSE
19	2050.5	32.1	510	2	Q80Y43_MOUSE
20	2048.5	32.1	1000	2	Q7TPI4_MOUSE
21	2011.5	31.5	779	2	Q7TOM9_MOUSE
22	2000	31.5	485	2	Q9BES5_RAT
23	1961.5	30.7	488	2	Q769E2_MOUSE
24	1945	30.5	1503	1	TRPM2_HUMAN
25	1945	30.5	1503	1	Q5KTC2_HUMAN
26	1896.5	29.7	1507	1	TRPM2_MOUSE
27	1894	29.7	1506	2	Q5G8C6_MOUSE
28	1886.5	28.6	1508	2	Q5G8E6_RAT
29	1813.5	25.8	803	2	Q4SHH2_TRYNG
30	1646.5	25.8	1095	2	Q5UK23_CHICK
31	1625.5	25.5	422	2	Q769E4_MOUSE

32	1612.5	25.3	1104	1	TRPM8_RAT	Q8r455	rattus norv
33	1608.5	25.2	1104	1	TRPM8_HUMAN	Q7z227	homo sapien
34	1606.5	25.2	1224	2	Q4RQ95_TRYNG	Q4RQ95	tetraodon n
35	1604	25.1	1289	1	Q5KTC1_HUMAN	Q5KTC1	homo sapien
36	1597.5	25.0	1104	1	TRPM8_MOUSE	Q8r4d5	mus musc
37	1462.5	22.9	567	2	Q6GPZ7_XENLA	Q6GPZ7	xenopus lae
38	1435	22.5	1709	2	Q5F4S7_MOUSE	Q5F4S7	mus muscu
39	1435	22.5	1718	2	Q692E8_MOUSE	Q692E8	mus muscu
40	1433.5	22.5	1732	1	TRPM3_HUMAN	Q9HCF6	homo sapien
41	1432	22.4	1721	2	Q5F4S9_MOUSE	Q5F4S9	mus muscu
42	1432	22.4	1721	2	Q5F4T0_MOUSE	Q5F4T0	mus muscu
43	1430.5	22.4	340	2	Q811E2_MOUSE	Q811E2	mus muscu
44	1429	22.4	1699	2	Q5F4S6_MOUSE	Q5F4S6	mus muscu
45	1426	22.3	1711	2	Q5F4S8_MOUSE	Q5F4S8	mus muscu

ALIGNMENTS

RESULT 1
Q8TD43_HUMAN PRELIMINARY; PRT; 1214 AA.
ID Q8TD43_HUMAN
AC Q8TD43;
DT 01-JUN-2002 (TRMBLrel. 21, Created)
DT 01-JUN-2002 (TRMBLrel. 21, last sequence update)
DT 01-FEB-2005 (TRMBLrel. 29, last annotation update)
DE Cation channel TRPM4B (Transient receptor potential ion channel
DE melastatin subgroup member 4 protein) (Transient receptor potential
DE cation channel subfamily M member 4 splice variant B).
GN Name=TRPM4; Synonyms=TRPM4B;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22011788; PubMed=12015988; DOI=10.1016/S0092-8674(02)00719-5;
RA Launay P., Fleig A., Peraldo A.L., Scharenberg A.M., Penner R.,
RA Kinet J.P.,
RT "TRPM4 is a Ca2+-activated nonselective cation channel mediating cell
RT membrane depolarization";
RL Cell 109:397-407(2002).
[2]
RA Pertaud A.-L., Scharenberg A.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22791733; PubMed=12799367; DOI=10.1074/jbc.M305127200;
RA Nilius B., Prenen J., Droogmans G., Voets T., Vennekens R.,
RA Freichel M., Wissenbach U., Flockerzi V.,
RL "Voltage dependence of the Ca2+-activated cation channel TRPM4";
RL J. Biol. Chem. 278:30813-30820(2003).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubandov V., Gudermann T., Montell C.,
RT "TRPM5 is a voltage-modulated and Ca2+-activated monovalent
RT selective cation channel";
RL Curr. Biol. 13:1153-1158(2003).
EMBL: AF497623; AM18083.1; -; mRNA.
EMBL: AF575813; CA05941.1; -; mRNA.
EMBL: AF297045; AAP4474.1; -; mRNA.
DR Ensembl: ENSG00000130529; Homo sapiens.
DR HGNC: HGNC:17993; TRPM4.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005261; F:cation channel activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:000612; F:cation transport; IEA.
DR Interpro: IPR002111; Cat_channel_TpL.
DR Interpro: IPR005821; Ion_trans.

DR Pfam; PF00520; Ion_trans; 1.
KW Receptor.
SEQUENCE 1214 AA; 134300 MW; 76ADA45269ED8F5 CRC64;
Query Match 100.0%; Score 6383; DB 2; Length 1214;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 M V P E K Q S W I P K I F K K K C T T F I V D S T D P G T L C Q C G R P T A H P A V A M E D A F G A A V V T V 60
DB 1 M V P E K Q S W I P K I F K K K C T T F I V D S T D P G T L C Q C G R P T A H P A V A M E D A F G A A V V T V 60
QY 61 W S D A H T T E K P T D A Y G E L D F T G A G R K H S N F L S D R T D P A A Y S L V T R T W G F R A P N L V V S 120
DB 61 W S D A H T T E K P T D A Y G E L D F T G A G R K H S N F L S D R T D P A A Y S L V T R T W G F R A P N L V V S 120
QY 121 V L G S G G P V L Q T W L D L R R G L V R A A Q S T G A M I V T G S L H T G I G R H V G V A V R D H O M A S T G G 180
DB 121 V L G S G G P V L Q T W L D L R R G L V R A A Q S T G A M I V T G S L H T G I G R H V G V A V R D H O M A S T G G 180
QY 181 T K V A M G V A P M G V V N R D T L I N P K G S F P A R Y R M R G D P E D G V P P L D Y N S A F L V D G T H 240
DB 181 T K V A M G V A P M G V V N R D T L I N P K G S F P A R Y R M R G D P E D G V P P L D Y N S A F L V D G T H 240
QY 241 G C L G G E N R F R L R E S Y I S Q O K T G V G T G I D I P V L L L I D G D E K M L T R I E N A T O A Q L P C L L 300
DB 241 G C L G G E N R F R L R E S Y I S Q O K T G V G T G I D I P V L L L I D G D E K M L T R I E N A T O A Q L P C L L 300
QY 301 V A G S G G A D C L A T I E D T L P A P S G G A R Q G E A R D I R F P F K G D L E V L Q A V E R I M T R K E L 360
DB 301 V A G S G G A D C L A T I E D T L P A P S G G A R Q G E A R D I R F P F K G D L E V L Q A V E R I M T R K E L 360
QY 361 L T Y V S S E D G S E E F E T I V L K A L V R A C S S E A S A Y L D E L R L A V A N R V D I A Q S E L F R G D I Q W 420
DB 361 L T Y V S S E D G S E E F E T I V L K A L V R A C S S E A S A Y L D E L R L A V A N R V D I A Q S E L F R G D I Q W 420
QY 421 R S F H L E A S L M D A L I N D R P E V R L L I S H G S L G H F L T P M R L A Q I Y S A P S N S L I R N L I D Q A 480
DB 421 R S F H L E A S L M D A L I N D R P E V R L L I S H G S L G H F L T P M R L A Q I Y S A P S N S L I R N L I D Q A 480
QY 481 S H S A G T K A P L K G S A E L R P D V G H V R M L I G M K C A P R Y S G A M D P H P Q G G E S W Y L L 540
DB 481 S H S A G T K A P L K G S A E L R P D V G H V R M L I G M K C A P R Y S G A M D P H P Q G G E S W Y L L 540
QY 541 S D K A T P L S I D A G I G A P W S D L L I M A L L I N R A Q M A Y F W E M G S N A V S A L G A C I L L R V N A 600
DB 541 S D K A T P L S I D A G I G A P W S D L L I M A L L I N R A Q M A Y F W E M G S N A V S A L G A C I L L R V N A 600
QY 601 R L E P D A B E A A R R K D L A F K F E G M G V D L F G E C Y R S S E V A A R L L R C P L M G D A T C L Q L A M Q 660
DB 601 R L E P D A B E A A R R K D L A F K F E G M G V D L F G E C Y R S S E V A A R L L R C P L M G D A T C L Q L A M Q 660
QY 661 A D R A R F P A D G V G S L L T O K W G D M A S T T P I W A L V I A F P C P L Y T L L I T F R K S E E P T T E 720
DB 661 A D R A R F P A D G V G S L L T O K W G D M A S T T P I W A L V I A F P C P L Y T L L I T F R K S E E P T T E 720
QY 721 E L E F D M D S V I N G S G P V G T A D P A E K T P L G V P R O S G R P C C G R C G R R C L R W H F M G A V 780
DB 721 E L E F D M D S V I N G S G P V G T A D P A E K T P L G V P R O S G R P C C G R C G R R C L R W H F M G A V 780
QY 781 T I F M G V N S Y L L F L L I P S R V L L V D P O P A P P G S I E L L L Y F M A F T L C B E L R O G I S G G G S S I 840
DB 781 T I F M G V N S Y L L F L L I P S R V L L V D P O P A P P G S I E L L L Y F M A F T L C B E L R O G I S G G G S S I 840
QY 841 A S G G P P G H A S L S O R L R I Y L A D S M N C D L V A L T C P L L G V C R L T P G I Y H L G R V L C I D P M 900
DB 841 A S G G P P G H A S L S O R L R I Y L A D S M N C D L V A L T C P L L G V C R L T P G I Y H L G R V L C I D P M 900
QY 901 V F T V R L L H I F T V N K O L G P K I V I S K M K O V F F L F L G V W L V A Y G A T E G I L R P R S D P P 960
DB 901 V F T V R L L H I F T V N K O L G P K I V I S K M K O V F F L F L G V W L V A Y G A T E G I L R P R S D P P 960
QY 961 S I I R R V Y R P Y I Q I F Q Q I P Q E D M D V A L M E H S N C S S B P G F M A P P G A Q A C T C V S Q V A N M I V 1020

DB 961 S I I R R V Y R P Y I Q I F Q Q I P Q E D M D V A L M E H S N C S S B P G F M A P P G A Q A C T C V S Q V A N M I V 1020
QY 1021 V L L V I F L V A N I L A V N L I A M F S Y T F G K V Q S D I Y M R A Q R Y L I R E F H S R P A L A P P F I 1080
DB 1021 V L L V I F L V A N I L A V N L I A M F S Y T F G K V Q S D I Y M R A Q R Y L I R E F H S R P A L A P P F I 1080
QY 1081 V I S H L R L L R Q L C R P R S P O S S P A L E H F R V I S K E A R K L T W S V H K E N F L L A D A R D K 1140
DB 1081 V I S H L R L L R Q L C R P R S P O S S P A L E H F R V I S K E A R K L T W S V H K E N F L L A D A R D K 1140
QY 1141 R E S D S R L K R T S Q K V D L A K O G I R E Y E O R L K V E R Y V Q O G S R Y T G W A E A L S R S A L I P 1200
DB 1141 R E S D S R L K R T S Q K V D L A K O G I R E Y E O R L K V E R Y V Q O G S R Y T G W A E A L S R S A L I P 1200
QY 1201 P G G P P P D L P G S K D 1214
DB 1201 P G G P P P D L P G S K D 1214
RESULT 2
Q725D9_HUMAN
ID Q725D9_HUMAN PRELIMINARY; PRT; 1069 AA.
AC Q725D9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Transient receptor potential cation channel subfamily M member 4
DE splice variant C.
GN Name=TRPM4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubakov V., Gudermann T., Montell C./
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent
RT selective cation channel."
RL Curr. Biol. 13:1153-1156(2003).
DR EMBL; AT297046; AAP44475.1; -; mRNA.
DR Ensembl; ENSG00000130529; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat_channel_TrypL.
KW Receptor.
SQ SEQUENCE 1069 AA; 118629 MW; 80DEBD935A55F200 CRC64;
Query Match 86.3%; Score 5505.5; DB 2; Length 1069;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 0; Indels 145; Gaps 1;
QY 1 M V P E K Q S W I P K I F K K K C T T F I V D S T D P G T L C Q C G R P T A H P A V A M E D A F G A A V V T V 60
DB 1 M V P E K Q S W I P K I F K K K C T T F I V D S T D P G T L C Q C G R P T A H P A V A M E D A F G A A V V T V 60
QY 61 W S D A H T T E K P T D A Y G E L D F T G A G R K H S N F L S D R T D P A A Y S L V T R T W G F R A P N L V V S 120
DB 61 W S D A H T T E K P T D A Y G E L D F T G A G R K H S N F L S D R T D P A A Y S L V T R T W G F R A P N L V V S 120
QY 121 V L G S G G P V L Q T W L D L R R G L V R A A Q S T G A M I V T G S L H T G I G R H V G V A V R D H O M A S T G G 180
DB 121 V L G S G G P V L Q T W L D L R R G L V R A A Q S T G A M I V T G S L H T G I G R H V G V A V R D H O M A S T G G 180
QY 181 T K V A M G V A P M G V V N R D T L I N P K G S F P A R Y R M R G D P E D G V P P L D Y N S A F L V D G T H 240
DB 181 T K V A M G V A P M G V V N R D T L I N P K G S F P A R Y R M R G D P E D G V P P L D Y N S A F L V D G T H 240
QY 241 G C L G G E N R F R L R E S Y I S Q O K T G V G T G I D I P V L L L I D G D E K M L T R I E N A T O A Q L P C L L 300

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2006, 08:55:56 : Search time 43 seconds

(without alignments)
2716.445 Million cell updates/sec

Title: US-09-869-486b-30

Sequence: 1 MVTPEKGGQWPKPKKTC.....RSALPPGGPPDPDPSKD 1214

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Lighting filter 45 summaries

Database:

1: PIR 80.*
2: p1r1.*
3: p1r2.*
4: p1r3.*
5: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1961.5	30.7	488	UC7995	transient receptor
2	1195.5	18.7	1868	T23707	hypothetical prote
3	1191.5	18.7	1400	T22644	hypothetical prote
4	1021.5	16.0	1707	T18951	hypothetical prote
5	248	3.9	899	P88391	protein R06810.4 (
6	247.5	3.9	1275	JU0092	trp protein - fru
7	246	3.9	1418	S40764	hypothetical prote
8	242	3.8	1274	JN0015	trp protein - fru
9	221.5	3.5	1124	JH0588	calmodulin-binding
10	209.5	3.3	823	S44873	zc21.2 protein - C
11	169	2.6	793	S68238	trp-1 protein - hu
12	169	2.6	810	T38361	TRPC1 protein - hu
13	167	2.6	828	JCS887	trp3 protein - rat
14	156	2.4	823	T34472	hypothetical prote
15	142.5	2.2	3413	T17467	riifamycin polypept
16	136	2.1	839	JC7621	cepaicicn receptor
17	133	2.1	675	T20822	hypothetical prote
18	132	2.1	456	H84278	hypothetical prote
19	128	2.0	245	AH2002	hypothetical prote
20	127	2.0	1245	E83110	exodeoxyribonuclea
21	125	2.0	509	G83442	probable 3-hydroxy
22	125	2.0	1255	T31065	diaphanous protein
23	123	1.9	5069	T17464	riifamycin polypept
24	119	1.9	542	T28688	hypothetical prote
25	118.5	1.9	790	T20312	hypothetical prote
26	118	1.8	970	E70533	probable sulfatase
27	118	1.8	2222	A37490	voltage-dependent
28	118	1.8	2272	C54972	voltage-dependent
29	117.5	1.8	3739	T17410	polyketide synthase

30	117.5	1.8	7463	2	T36248	CDA peptide synthe
31	116.5	1.8	727	2	UC7796	epithelial calcium
32	116.5	1.8	1876	2	C70749	probable ppa prot
33	116.5	1.8	7576	2	T17428	FK506 polypeptide s
34	116	1.8	765	2	H70763	probable glycy prot
35	116	1.8	900	2	T33026	hypothetical prote
36	116	1.8	1997	2	T30874	virginiamycin S by
37	116	1.8	2178	2	S29237	calcium channel pr
38	116	1.8	2259	2	S29236	calcium channel pr
39	115.5	1.8	838	2	T09054	cepaicicn receptor
40	115.5	1.8	1438	2	T17402	dihydroerginotol
41	115.5	1.8	1728	2	T17466	riifamycin polypept
42	115	1.8	598	2	B75626	PTS system, fructo
43	115	1.8	881	2	T03461	methyl-accepting c
44	114.5	1.8	735	2	T35778	probable fusidic a
45	114.5	1.8	854	2	T23155	hypothetical prote

ALIGNMENTS

RESULT 1	
UC7995	transient receptor potential potential-melastatin 4 channel - mouse
C/Species:	Mus musculus (house mouse)
C/Date:	10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C/Accession:	UC7995
R/Murakami, M.; Xu, F.; Miyoshi, I.; Sato, B.; Ono, K.; Iijima, T.	
Biochem. Biophys. Res. Commun. 307, 522-528, 2003	
A/Title:	Identification and characterization of the murine TRPM4 channel.
A/Reference number:	UC7995; PMID:12893253
A/Accession:	UC7995
A/Molecule type:	DNA
A/Residues:	1488 <MUR>
A/Cross-references:	GB:NM000319
A/Experimental source:	Brain, C57/BL6
A/Comment:	This protein, a member of subfamily of transient receptor potential channels,
A/Genes:	trpm4
A/Map position:	7B2
A/Intons:	12/2, 153/2, 197/3, 256/1, 315/2, 384/1, 428/2, 452/3
C/Keywords:	calcium entry; transient receptor potential; transmembrane domain; TRPM
Query Match	
Best Local Similarity 30.7%; Score 1961.5; DB 2; Length 488;	
Matches 384; Conservative 32; Mismatches 66; Indels 13; Gaps 5;	
QY	726 MDSVINGEGPVTADPAKPTPLGVPRQSGPG---CCGRCGGRCLRRFHWGAPVTI 782
DB	1 MDSINGAGPPTVPEPAKVAL-ERRQRAPGRALCCG-----KFSKMSDFGAPVTA 53
QY	783 FMGNVSYLLFLFLFSVLLVDFOPARPGLELLIYMAATTLCELRQISGGGSLAS 842
DB	54 FLGNVSYLLFLFLFAVLLVDFQPTPSVSELLIYMAATTLCELRQISGGGSLAS 113
QY	843 GSGPGHASSORLRLYLADSNOCDLVALTCFLIAGVCLTRPLYHIGRTVLCIDPMVF 902
DB	114 GSGPDRAPRLRRLHLYLSTNOCDLALTCFLIAGVCLTRPLRPLGRTVLCIDPMIF 173
QY	903 TVRLHLFTVNKOLGPKIVIVSRMKDVFFFLFGLGVMLVAYGVAATGGLRPDSDFPSI 962
DB	174 TVRLHLFTVNKOLGPKIVIVSRMKDVFFFLFGLGVMLVAYGVAATGGLRPDSDFPSI 233
QY	963 LRRVFRPYQIQGQIQGEMDVALMHSHSCSSRPGFWAPRPAQAQCTCQVANNIVL 1022
DB	234 LRRVFRPYQIQGQIQGEMDVALMHSHSCSSRPGFWAPRPAQAQCTCQVANNIVL 293
QY	1023 LTVFLVANNILVNLIAFSTYFGKQNSDLYWTAQRYRLIRRHSPALAPPIVI 1082
DB	294 LTVFLVANNILVNLIAFSTYFGKQNSDLYWTAQRYRLIRRHSPALAPPIIII 353
QY	1083 SHRLRLRLQ--CNR-PRSDQSSPALRRFRVYLKSKERKLLTWSEVKNFTLADARD 1139

Db 354 SHVRLIKWLRRRCRRANLPA5PVEHFRVCLISKEAEKLLTWESVHKENFLLAQARD 413
QY 1140 KRESDESRLKRTSQKVDLALKQJHIREYECRLKVLEREYQCCSVLGVAAALSSALL 1199
Db 414 KRSDSRLKRTSQKVDLALKQJHIREYECRLKVLEREYQCCSVLGVAAALSSALL 473
QY 1200 PEGGPPPPDLPGSKD 1214
Db 474 PPGAPPPPPPTGSKD 488
RESULT 2
T23707
hypothetical protein T01H8.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_rev15ion 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T23707; T24342
R:Kerhaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19786
A:Accession: T23707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 11868 <M1868>
A:Cross-references: UNIPARC:UPI000017BB41; EMBL:Z83117; PIDN:CA805572.1; GSPDB:GN00019;
A:Experimental source: clone M04C7
R:Lenhard, N.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19877
A:Accession: T24342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1868 <M1868>
A:Cross-references: UNIPARC:UPI000017BB41; EMBL:Z80219; PIDN:CA802303.1; GSPDB:GN00019;
A:Experimental source: clone T01H8
C:Genetics:
A:Gene: CESP:T01H8.5
A:Map position: 1
A:Insertions: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1
Query Match 18.7%; Score 1195.5; DB 2; Length 1868;
Best Local Similarity 24.8%; Pred. No. 2e-81;
Matches 385; Conservative 233; Mismatches 499; Indels 431; Gaps 51;
QY 9 SWIPKIFKKKCTCTTPTVSDTDPGGLCQCGRPRTAH-----PAVAMEADAF 53
Db 118 NWREFTREGRFCLASSRD--HKCGGRTDAHNIPELSBFLQKRSVALAQOR 175
QY 54 GAANVT-----VWSDAHTTEKPTDAVGEIDFTTGAGRKH-SNPLRLSDR 96
Db 176 SLENVNDINTOMMYTKGANKEMKSLRKHTVSLATNAPFGQVEFGGPHPKAQYVRVNP 235
QY 97 TDAAYVSVITRTWGPAPVLLVSVYGGSGPVLQTMLODLRRGLVRAQSGAMITVG 156
Db 236 TBAAYMSLSEHAWQJSPRLIITVHGGSINFDLPRLAVFRKGLKALASTIGAMITIS 255
QY 157 GLHTGIGRHVAVNRDHQMASTGGTKVAVGAPVWGVNRDILINPKGSFP-----ARY 211
Db 296 GCGTGVKVAALLEGASQNR--NKIVCIGIAPWGLLKRGEDFIGDDKVPYRPSKSG 353
QY 212 RWRGDEPDGVQPLVDVYSAFPLVDDGTHGCLGSENRFLRLSEYSIOQKTVGGTIGDI 271
Db 354 RFTG-----LNNHSYFLLVDNGTVGRYGAELVLRKLEMYISQKOKIFGTR-SV 403
QY 272 PVLILLIDG-----EKMLTINATQAQLPCLLVASGGAADCLA-----ETLEDTLAPGS 323
Db 404 PVVCVAVLEGSSCTIRSVLDVYTVN--PRVAVVCDGSGRADLILAPAHQNTVEDGLP-- 459
QY 324 GGARQGEARDIRRFKGLDLEVL-----QKQVERIM-----TRKELLTVYS- 365
Db 460 -----DDIR-----QVLLVETTFGCSBAARHLHLBELVCAQHKLTLITFRL 503
QY 366 SEDGSEEFETTVLKALVYKACSSBAAYLDELRLAVANRVDTAQSELFRGDIQMRSPHL 425

Db 504 GEQGEHDVHALITALLKQNTLSA-----DQALALAMRVDTIARSDVFMGHEWQAL 529
QY 426 EASIDALINDREPRRLIISHGLSGLFTPLRLALQYSA--APNSILRLINDQASHS 483
Db 560 HNAEMELIHDRVDFRLILLEGQINNOKFLTISRDELVNTDGPENTLEFYIRDVVR 619
QY 484 AGTKAPALKGAAELRPDPVGHVRLMLGKMCAPRY----- 519
Db 620 QGYR-----FLPDIGLVIEKLMGNSYQCSYTSSEFRDKYQRMKRVGHAQKAM 669
QY 520 -----PS-----GGA-----WDHPH----- 529
Db 670 GVFSSRPSRTSGSIASRQSTEGKGVGVGGSVAQVFGNSFGNODPPLDPVHNSALSGR 729
QY 530 -----GQGFGEAMVLLSDKATSPSLDAGLQGA 557
Db 730 ALSNHILMRSAPRGNPRANPRPNLGDSDGSEDELSLSADSGQTEBDF--RY 786
QY 558 PMSDLLMALLLNRAQAMAYFWEMGSNAVASALQACLLIRVAMRLP---DAEAPARK 613
Db 787 PYSELMIMAVLTFKQDMACMOMQHGEAMAKALVACRLYKSLATEBAEDYLEVEICEBK 846
QY 614 DLAFKBEKGVULFGECSSESVRARLLRRCPLMGDNTCLQAMQADARAFADGVQ 673
Db 847 KXAEFRILSLDLHCYHVDACQTLQTLTVELSNNSNFCALAVIVNNKFLHAPCCQ 906
QY 674 SLTQKMGDMASTT-PVALVYAFPCPLIYTRLTTPKRSSE--EP-TRESELRDMD- 727
Db 907 ILLADIMHGLMRHTSNIKVILGILCPPI--QMELFTREELINQPGTAAEHQNDMAY 964
QY 728 -----SVINGEFGVTADPA-----EKTPLG----- 748
Db 965 SSSSSSSSSSSSSSSSSSSSSFEEDDDENNAHNDQKTRKTSQSGAQSINITSLFHSR 1024
QY 749 -----VPROSGRGCCGG-----RCGGR----- 766
Db 1025 RAKKNEKCDRETDASACAGNRQIQNGGLTABYGTGSGNGVSPPPPTMRANSRRRYNN 1084
QY 767 -----RCLRRMFHFWGAPVT 782
Db 1085 RSDMSKTSVIRGSDPNLSKLQKSNITSTDRNPMQPGTKRIKRRRFYEYSAPIS 1144
QY 783 FNGNVSVYLLFLLESRLVLDOPAPGSLR--LLIYFWAFLTLCBELRQGLSGGGSL 840
Db 1145 FMSWTISFLITFTFYTLTTPPRPT-VIEYILAVYAAAGL--EQVRKII-----M 1195
QY 841 ASGGPGRGASLSQRLRLVLDMSWNOCDLVALTCLPLGVGCRUTPGLYHGLRTVLCIDPM 900
Db 1196 SDAKP-----FYEKIRTVCSFPMNCVTTLALITFYVGFPMRCF-GSVAAYGYILACDV 1248
QY 901 VFTVRLHIFTVVKQJGPKIVISKMKDVFPFLPFLGVYLVAYGVATEGLRPRDSDP 960
Db 1249 LWTMKLDVMSVHPKGLFVYVMAKMIQMSAYIIVLVLTLSFGIARSTIYRDBTWM 1308
QY 961 SIIRRVFRPYQIQFQIPQEDMDVALMHSNCSSEPGWAA-----PRGAQAGT 1010
Db 1309 ILVRNIFLRFYMLVGEVYADEID-----TCGBEA--WDHLENGSGVILGNGTGTGS 1359
QY 1011 CYSQVANNMLVLLVILVAVNILLVNLILAMPSTYFGVQNSDLVYKARVRLRBFH 1070
Db 1360 CVPGY--WIPLLMTFFLLIANILMSMLIAFNHIFDATDMSQGIWLPQRKQWMEYS 1417
QY 1071 SRPALAPPIVISHRLTL-----RQLCRPRSPQSPSPALBHFVYLSKEARKLLTW 1125
Db 1418 STPLPPLPLTLYHGLIIGFTRILSCSGSGERNITL-LIKAIELFLNDQIEKLDHE 1476
QY 1126 SVHKNELLARADKRESDESLKRTSQVDLALQKL-----GHIREYORLKY 1174
Db 1477 BOCMEDLQAKNEKNTSNEGRILLRADIRTDQILNRLIDLOAKESWGRDVINDVESRLAS 1536
QY 1175 LRR---EVQCCGRVL---GWVAELSRSLALP-----GGPPP---DLPGS 1212

CC extracellular calcium influx into their SOC/CRAC-expressing cells. They
 CC will also be useful for delivering therapeutic and/or imaging agents to
 CC such cells to modulate proliferation and growth. SOC/CRAC polypeptides
 CC also represent targets for designing and/or identifying inhibitors that
 CC block lymphocyte proliferation and binding agents that selectively bind
 CC to SOC/CRAC polypeptides to which drugs or toxins can be conjugated for
 CC delivery to SOC/CRAC expressing cells. Methods for determining the level
 CC of SOC/CRAC expression in a subject can be used to assess the presence,
 CC or absence, or stage of a proliferative disorder, e.g. a lymphocyte
 CC proliferative disorder

XX Sequence 1214 AA;

Query Match 100.0%; Score 6383; DB 3; Length 1214;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPBEKQSWI PKI FKKKCTTPIVDSTDPGGTLCCGGRPTAHPAVAMEDAFGAAYTV 60
 DB 1 MNPBEKQSWI PKI FKKKCTTPIVDSTDPGGTLCCGGRPTAHPAVAMEDAFGAAYTV 60
 QY 61 WDSDAHTTEKPTAYGELDTGAGRKSNFLRSDRDPAAVYSLVTRTWGFPAPNLVVS 120
 DB 61 WDSDAHTTEKPTAYGELDTGAGRKSNFLRSDRDPAAVYSLVTRTWGFPAPNLVVS 120
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 DB 121 VLGGSGPVLQTMLODLIRGLVRAAOSTGAMITVGTGIGRHVGAARVADHOMASTGC 180
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 DB 121 VLGGSGPVLQTMLODLIRGLVRAAOSTGAMITVGTGIGRHVGAARVADHOMASTGC 180
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 DB 181 TKVAVGVAVPWGVVNRDITLINPKSFPARYRMGRDEPDGVPELDVNYSAFPLVDDGTH 240
 QY 241 GCLGGERPFLRLSESYISQOKTGVGTGIDIPVLLLIIDBEKLTPIENATQALPCLL 300
 DB 241 GCLGGERPFLRLSESYISQOKTGVGTGIDIPVLLLIIDBEKLTPIENATQALPCLL 300
 QY 241 GCLGGERPFLRLSESYISQOKTGVGTGIDIPVLLLIIDBEKLTPIENATQALPCLL 300
 DB 241 GCLGGERPFLRLSESYISQOKTGVGTGIDIPVLLLIIDBEKLTPIENATQALPCLL 300
 QY 301 VAGSGAADCIAETLEDTLAPGSGAQRGEARDIRRFPPKGDLEVLQAVERIMTKEL 360
 DB 301 VAGSGAADCIAETLEDTLAPGSGAQRGEARDIRRFPPKGDLEVLQAVERIMTKEL 360
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 DB 301 VAGSGAADCIAETLEDTLAPGSGAQRGEARDIRRFPPKGDLEVLQAVERIMTKEL 360
 QY 361 LTVYSSSEDSSEBPETIYLKALVKACSSSEASAYDELRLAVANRVDAIOSBLFRGDIO 420
 DB 361 LTVYSSSEDSSEBPETIYLKALVKACSSSEASAYDELRLAVANRVDAIOSBLFRGDIO 420
 QY 421 RSFHLASLMDALLNDRPEFVRLIISHGLSHGLTWMRLAQLYSAPNSILRNLLDOA 480
 DB 421 RSFHLASLMDALLNDRPEFVRLIISHGLSHGLTWMRLAQLYSAPNSILRNLLDOA 480
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 DB 481 SHSAGTKAPALKGAALRPPDVGVRLMLLKKACARYPSGAMDPHPOGFGESMYLL 540
 QY 541 SDRKATSPSLIDAGLGQA PMSDDLIMALLNRAQAAVYFWEMGSAVSSALGACILLRVMA 600
 DB 541 SDRKATSPSLIDAGLGQA PMSDDLIMALLNRAQAAVYFWEMGSAVSSALGACILLRVMA 600
 QY 601 RLEPDAEBAARRDLAKFPEGMGVDLFGECYRSSEVAAARLLLRCLMNDATCLOLAMO 660
 DB 601 RLEPDAEBAARRDLAKFPEGMGVDLFGECYRSSEVAAARLLLRCLMNDATCLOLAMO 660
 QY 661 ADARAFAPADQVOSLITQKMGDMASTPIWALVAFPCPELITRLITRKSEEBETRE 720
 DB 661 ADARAFAPADQVOSLITQKMGDMASTPIWALVAFPCPELITRLITRKSEEBETRE 720
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QY 841 ASGSGPGRHANSORLRLYLADSWNOCDLVALTCFLGVCRLTPGLYHLGRTVLCIDFM 900
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 QY 1201 PGSPPEPDLPGSKD 1214
 DB 1201 PGSPPEPDLPGSKD 1214

RESULT 2
 ADH62712
 ID ADH62712 standard; protein; 1214 AA.

ADH62712;

25-MAR-2004 (first entry)

Ca activated nonselective transmembrane channel protein TRPM4b.

bioactive agent; monovalent cation permeability; TRPM4b channel; human;

calcium activated nonselective transmembrane channel.

Homo sapiens.

US2003143557-A1.

31-JUL-2003.

08-MAY-2002; 2002US-00142649.

25-JAN-2002; 2002US-0351938P.

02-MAY-2002; 2002US-0377937P.

(PENN/) PENNER R.

Penner R;

WPI; 2003-829785/77.

N-PSDB; ADH62711.

Screening for candidate bioactive agents involves contacting calcium-

activated nonselective transmembrane channel polypeptide designated as

TRPM4b with candidate agent, determining binding of candidate agent

TRPM4b.

Claim 4; SEQ ID NO 2; 25pp; English.

The invention describes a method of screening (M1) for a candidate

bioactive agent (CA) modulating monovalent cation (MC) permeability of

the TRPM4b (I) channel. The method involves providing a recombinant cell

(RC) with a nucleic acid encoding (I) and an inducible promoter operably

linked to (I), capable of expressing (I), and comprises an MC indicator,

inducing RC to express (I), contacting RC with MC and CA, and detecting

No.	Score	Query	Match	Length	DB	ID	Description
1	2158	75.7	3118	11	D0031081	D0031081	Homo sapi
2	2228.8	67.2	2532	11	D0031082	D0031082	Pan trogl
3	1983	54.4	4293	4	AK040094	AK040094	Mus muscu
4	773.6	21.2	912	6	CA488162	CA488162	AGENCOURT
5	719	19.7	879	5	B0858032	B0858032	AGENCOURT
6	697.4	18.1	700	7	CN002589	CN002589	170004706
7	690	18.9	933	5	BQ942718	BQ942718	AGENCOURT
8	666	18.3	894	5	BQ721564	BQ721564	AGENCOURT
9	651.6	17.9	883	5	B0723742	B0723742	AGENCOURT
10	646.8	17.8	864	6	CA488864	CA488864	AGENCOURT
11	644.4	17.7	862	7	CJ031569	CJ031569	CJ031569
12	637.4	17.5	1090	2	BF311509	BF311509	601897749
13	634.4	17.4	672	3	BI759746	BI759746	603045620
14	609.8	16.7	613	5	BK474984	BK474984	DXR2P686M
15	595.4	16.3	804	2	BB905591	BB905591	601495244
16	594.4	16.3	3449	4	AK035197	AK035197	Mus muscu
17	594.4	16.3	3598	4	AK044908	AK044908	Mus muscu
18	592.2	16.3	859	7	CJ023247	CJ023247	CJ023247
19	584.8	16.1	625	2	BI199159	BI199159	602758878
20	580.2	15.9	599	7	BI910079	BI910079	603067915
21	579	15.9	602	7	CN402548	CN402548	170005322
22	578	15.9	3498	10	AY401205	AY401205	Homo sapi

23	577	15.8	580	3	BP265210	BP265210
24	577	15.7	997	2	BP10664	BP10664
25	568	15.6	587	2	BI010535	BI010535
26	560	15.4	892	5	BQ949247	BQ949247
27	551	15.1	553	7	CN402551	CN402551
28	550.4	15.1	574	8	DR003765	DR003765
29	527	14.5	725	8	CK955668	CK955668
30	526	14.4	551	6	CB266373	CB266373
31	521	14.3	582	3	BP3511258	BP3511258
32	519.2	14.3	751	7	CJ031892	CJ031892
33	509	14.0	582	3	BP280941	BP280941
34	504.8	13.9	678	3	BP238875	BP238875
35	499.2	13.7	540	7	CN335029	CN335029
36	497.4	13.7	895	5	BQ918283	BQ918283
37	495	13.6	519	2	BI198663	BI198663
38	485.4	13.3	732	7	CO248115	CO248115
39	483	13.3	483	3	BO084154	BO084154
40	482.4	13.2	780	8	BU610616	BU610616
41	478	13.1	698	8	DN935772	DN935772
42	466	12.8	759	7	CO245095	CO245095
43	463.8	12.7	3483	10	AY401107	AY401107
44	457.6	12.6	611	2	BE313619	BE313619
45	453.8	12.5	465	7	CN402550	CN402550

ALIGNMENTS

RESULT 1
DO031081

DO031081

C119 L= RUN 14-NOV-66 CCG 03-TM-2005

DEFINITION	Homo sapiens TRPM4 gene, partial sequence genomic survey sequence.	VIRTUAL TRANSCRIPT , partial sequence
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VERSION DQ031081.1 GI:66882
KEYWORDS GSS.

ORGANISM *Homo sapiens*

Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS
Nielsen, R., Bustamante, C., Clarn, A. G., Glanowski, S., Sackton, T. B.,
Hubisz, M. J., Fedel-Alon, A., Tatenbaum, D. M., Civeello, D.,

TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

PUBMED 15869325
REFERENCE 2 (bases 1 to 3118)

Hubisz, M.J., Fiedel-Alon, A., Tatenbaum, D.M., Civello, D., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.

JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive
Rockville, MD 20850, USA

them based on alignment. Translation starts at the beginning of alignment.

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1. .3118
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/gene="TRPM4"  
/locus tag="HC814"
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Query Match 75.7%; Score 2758; DB 11; Length 3118

Matches 2758; Conservative 0; Mismatches 360; Indels 0; Gaps 0.

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DB 1 ATGGCCAGCACTGGGGGACCAAGTGTGACCATGGGTGGCCCCCTGGGGTGTGCTC 60
QY 583 CGGAATAGAGCACCTTCATCAACCCCAAGGCTCTGTTCCCTGGAGGTACCGGTGGGC 642
DB 61 CGGAATAGAGCACCTTCATCAACCCCAAGGCTCTGTTCCCTGGAGGTACCGGTGGGC 120
QY 643 GGTGACCCGAGAGACGGGGGTCAAGTTTCCCTGACCTACACTAGCGGCTTCTCTG 702
DB 121 GGTGACCCGAGAGACGGGGGTCAAGTTTCCCTGACCTACACTAGCGGCTTCTCTG 180
QY 703 GTGACGACGGGACACAGGCTGCTGGGGGGCGAGAACCGGCTTCCGCTTCCGCTGGAG 762
DB 181 GTGACGACGGGACACAGGCTGCTGGGGGGCGAGAACCGGCTTCCGCTTCCGCTGGAG 240
QY 763 TCCATCATCTCAACAGCAAGAAAGCGGGCTTGGAGAGGACTGGAATTGACATCCCTGTCTG 822
DB 241 TCCATCATCTCAACAGCAAGAAAGCGGGCTTGGAGAGGACTGGAATTGACATCCCTGTCTG 300
QY 823 CTCCTCCGATTGATGTGATGAGAGATGTTGACGCGAATGAGAACGCCACCGAGCT 882
DB 301 CTCCTCCGATTGATGTGATGAGAGATGTTGACGCGAATGAGAACGCCACCGAGCT 360
QY 883 CAGCTCCCATGTCTCTTGTGGCTGCTCAGGGGGAGCTGGGACTGCTGGCGAGACC 942
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QY 943 CTGGAACACACTCTGGCCCCGAGAGTGGGGGACCGAGGCAAGGCCGAAAGCCCGAGATCGA 1002
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QY 1003 ATCAGGGTTTCTTCCCAAGGGGACCTTGAAGTCTCTGACGGGCCAGGTGAGAGATT 1062
DB 481 ATCAGGGTTTCTTCCCAAGGGGACCTTGAAGTCTCTGACGGGCCAGGTGAGAGATT 540
QY 1063 ATGACCCGGAAGAGCTCTGACAGTCTATTCTTCTGAGAGTGGGTCTGAGAAATTCGAG 1122
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DB 841 CTGACCCCGAATGCGCTGTGACCACTCTACAGCGCGGCGCTTCAACTGCTCATCGC 900
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DB 901 AACCTTTTGAACAGCGGTCTCCACAGCGGAGGACCAAGGCCCAAGCCCTTAAAGGGGGA 960
QY 1483 GCTGCGAGACTCTCGGCCCCCTGAGAGTGGGGGATGTGCTGAGAGATGCTGTGGGGAATG 1542
DB 961 GCTGCGAGACTCTCGGCCCCCTGAGAGTGGGGGATGTGCTGAGAGATGCTGTGGGGAATG 1020
QY 1543 TGGCGCGAGGTAACCTCTCGGGGGGCGCTGTGACCTCAACCCAGGCAAGGGCTTGGGG 1602
DB 1021 TGGCGCGAGGTAACCTCTCGGGGGGCGCTGTGACCTCAACCCAGGCAAGGGCTTGGGG 1080

QY 1603 GAGAGCATGTATCTGCTCTGGAACAAGGCCACTCGCCGCTCTGCTGATGTCTGGCTC 1662
DB 1081 GAGAGCATGTATCTGCTCTGGAACAAGGCCACTCGCCGCTCTGCTGATGTCTGGCTC 1140
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DB 1141 GGGAGGCCCCCTGGAAGGACCTGCTCTTGTGGGCACTGTTGTGAAACAAGGCAAGATG 1200
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QY 1963 CTCAGCTGGCACATGCAAGCTGACGCGCTGTCTTGTGCGCAGATGGGTTACAGTCT 2022
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QY 2023 CTGCTGACAGAAATGTGTGGGAGATATAGGACAGCATCAACCATGTGGGCTGTGTT 2082
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DB 1561 CTCGCTTCTTTTGCCTTCACTCATCTACACCGCTCATCACTTCAAGAAATCAGAA 1620
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DB 1741 GGTCCGGGTTGTGCGGGGGGCGCTGTGGGGGCGCGGTCCTACGCGCTGTGTTTAC 1800
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QY 2383 CTGCTTTTCTGGGGGTTGCTGTGAGATTTTCAAGCGGGGCGCGGCTCCCTGGAG 2442
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QY 2443 CTGCTCTTATTTTGGGCTTTTCAAGCTGTGTGCGAGGAACTGCGCCAGGCTGAGC 2502
DB 1921 CTGCTCTTATTTTGGGCTTTTCAAGCTGTGTGCGAGGAACTGCGCGGCTGAGC 1980
QY 2503 GGAAGCGGGGGGACGCTCGCAAGCGGGGGCTCGGGGCTGTGCCATGTCTCATGAGCAG 2562
DB 1981 GGAAGCGGGGGGACGCTCGCAAGCGGGGGCTCGGGGCTGTGCCATGTCTCATGAGCAG 2040
QY 2563 GGCCTGGCTCTAACCTGCGCGACAGCTGGAACAAGTGACACTTATGTGCTCACTGC 2622
DB 2041 GGCCTGGCTCTAACCTGCGCGACAGCTGGAACAAGTGACACTTATGTGCTCACTGC 2100
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DB 2101 TTTCTCTGGGCGTGGGCTGCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2160
QY 2683 CTCTGATGACATTTCATGTTTTCAGAGTGGGCTGCTTCACATTTACGTTCAACAAA 2742

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OY	2545	CATGCGCTCATGAGCCAGGCGCTCGCGCTTACCTTCGCGGACAGCTGGAACCATGCGAC	2604
Db	70	CATGCGCTCATGAGCCAGGCGCTTCGGCCCTTACCTTCGCGGACAGCTGGAACCATGCGAC	129
OY	2605	CTAGTGGCTCTCAGCTGCTTCTCTCTGGGCGTGGGCTGCGCGGCTGACCCCGGATTGTAC	2664
Db	130	CTAGTGGCTCTCAGCTGCTTCTCTCTGGGCGTGGGCTGCGCGGCTGACCCCGGATTGTAC	189
OY	2665	CACCGGGGCGGCACTGCTCTCGAATGACCTTCAAGTATTTCAAGGATGGGCGTCTTAC	2724
Db	190	CACCGGGGCGGCACTGCTCTCTCGAATGACCTTCAAGTATTTCAAGGATGGGCGTCTTAC	249
OY	2725	ATCTTCACGGTCAACAAACAGCTGGGGGCCAAGATCGTCACTGATGACAAATGATGAG	2784
Db	250	ATCTTCACGGTCAACAAACAGCTGGGGGCCAAGATCGTCACTGATGACAAATGATGAG	309
OY	2785	GAAGTATCTTCTCTCTCTCTCTCTCTCGGCGTGGGCTGGTACCTATGCGTGGCCAGC	2844
Db	310	GAAGTATCTTCTCTCTCTCTCTCTCTCGGCGTGGGCTGGTACCTATGCGTGGCCAGC	369
OY	2845	GAGGGGCGCTCGAGGGCCAGGGGACAGTACCTTCCCAATATCTGGCGCGCGCTTTCAC	2904
Db	370	GAGGGGCGCTCGAGGGCCAGGGGACAGTACCTTCCCAATATCTGGCGCGCGCTTTCAC	429
OY	2905	CGTCCCTCATCTGCACATCTTCGGGACAGATTCCCGAGAGGACATGAGCGTGGCCTCATG	2964
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Db	490	GAGCACAGCAACTGCTCGTGGGAGCCGGGCTTCTGGGCAACCCCTCTGGGGCCCAAGCG	549
OY	3025	GGCACCTGGCTCTCCCAATATGCCACCTGGCTGGTGGTGGTCTCTCTCATCTTCTG	3084
Db	550	GGCACCTGGCTCTCCCAATATGCCACCTGGCTGGTGGTGGTCTCTCTCATCTTCTG	609
OY	3085	CTCGGGGCAACATCTCTGGTCAACTTGGCTCATTTGCGATGTTACATTCAGC	3144
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Db	850	TTCCGGGTTTACCTTCTTAAGGAAGCCAGGCGGAAGCTCTAAGGTGGAAATCGGTGAT	909
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Db	910	AAGGAAACTTTCTGTGGCAACGCGCTAAGGAACAAGCGGAGAGCGAATCCGAGCGTGG	969
OY	3445	AAGGCAACGTCCCAAGATGGAATTTGGCACTGAAACAGCTGGGAACAATCCGGAGATAC	3504
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		/ Patent No. 6262245		
		GENERAL INFORMATION:		
		APPLICANT: Xu, Jiangchun		
		APPLICANT: Dillon, Davin C.		
		TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO		
		NUMBER OF SEQUENCES: 224		
		CORRESPONDENCE ADDRESS:		
		ADDRESSEE: SEED AND BERRY LLP		
		STREET: 6300 Columbia Center, 701 Fifth Avenue		
		CITY: Seattle		
		STATE: WA		
		COUNTRY: USA		
		ZIP: 98104		
		COMPUTER READABLE FORM:		
		MEDIUM TYPE: Floppy disk		
		COMPUTER: IBM PC compatible		
		OPERATING SYSTEM: PC-DOS/MS-DOS		
		SOFTWARE: Patent In Release #1.0, Version #1.30		
		CURRENT APPLICATION DATA:		
		APPLICATION NUMBER: US/09/030,607		
		FILING DATE: 25-FEB-1998		
		CLASSIFICATION:		
		ATTORNEY/AGENT INFORMATION:		
		NAME: Makl, David J.		
		REGISTRATION NUMBER: 31,392		
		REFERENCE/DOCKET NUMBER: 210121.427c3		
		TELECOMMUNICATION INFORMATION:		
		TELEPHONE: (206) 622-4900		
		TELEFAX: (206) 682-6031		
		INFORMATION FOR SEQ ID NO: 109:		
		SEQUENCE CHARACTERISTICS:		
		LENGTH: 1524 base pairs		
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		STRANDEDNESS: single		
		TOPOLOGY: linear		
		MOLECULE TYPE: cDNA		
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		ORGANISM: Homo sapiens		
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Db		130	CTAAGGAGCTCACCTGCTTCCTCTGCGGCGTGGGCTGCGGACTGACCCCGGATTGTAC	189
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 09:03:31 ; Search time 1922 Seconds

(without alignment)
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Gapop 10.0 , Gapext 1.0

Searched: 496997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Printing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	3642	100.0	4061	13	ADSI2774
6	3642	100.0	4061	14	ADV97224
7	3640.4	100.0	4042	6	AAJ32372
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34	1158	31.8	1524	2	AAV61200	AAv61200 Full leng
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36	1158	31.8	1524	3	ABSI7253	ABsi7253 Human pro
37	1158	31.8	1524	4	AAH93464	AAh93464 Human pro
38	1158	31.8	1524	4	AAH63556	AAh63556 Human pro
39	1158	31.8	1524	4	AAH02529	AAh02529 Prostate
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ALIGNMENTS

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AC		
XX		
DT	24-MAR-2005	(first entry)
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DB	TRPM4 coding sequence, SEQ ID 15.	
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KM	Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; gene; ss.	
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OS	Homo sapiens.	
XX		
PN	WO2005001092-A2.	
XX		
PD	06-JAN-2005.	
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PF	19-MAY-2004; 2004WO-US015645.	
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PR	20-MAY-2003; 2003US-0471729P.	
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PI	Be X, Wei L, Slonim DK, Howes SH;	
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XX	WPI; 2005-075568/08.	
DR	P-PSDB; ABR99976.	
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PT	Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABC4, or a T cell	
PT	activated by the polypeptide or antibody, and a carrier, useful for	
PT	treating cancer.	
XX		
PS	Claim 8; SEQ ID NO 15; 113pp; English.	
XX		
CC	The present invention relates to a novel pharmaceutical composition	
CC	comprising: (a) an agent capable of modulating an expression level or	
CC	protein activity of a cancer-related transmembrane protein (CRTP) or gene	
CC	; an antibody specific for a CRTP, or a T cell activated by a CRTP; and	
CC	(b) a carrier. The pharmaceutical composition may also comprise a	
CC	polynucleotide capable of inhibiting or decreasing the expression of the	

CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPM34, HAVCR1, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is
CC the coding sequence for one such CRTP. Note: The sequence data for this
CC in electronic format part of the printed specification, but was obtained
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 4001 BP: 689 A: 1253 C: 1275 G: 784 T: 0 U: 0 Other:

Query Match 100.0%; Score 3642; DB 14; Length 4001;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1193	CTTGTGAAGGCTGTGGAGCTGGAGGCGCTCAGCGCTACCGATGAGCTGCGTTGGCT	1252
QY	1201	GTGCTTTGAAACCGCGTGAACATTGCCAGAGTGAATCTTTTGGGGGGAACATTCATYGG	1260
Db	1253	GTGCTTTGAAACCGCGTGAACATTGCCAGAGTGAATCTTTTGGGGGGAACATTCATYGG	1312
QY	1261	CGGCTCTTCATCTCGAAGCTTCCCTCAATGAGCGCTGCTGAATGACCGGCGTAGTTC	1320
Db	1313	CGGCTCTTCATCTCGAAGCTTCCCTCAATGAGCGCTGCTGAATGACCGGCGTAGTTC	1372
QY	1321	GTGCGCTTGTCAATTTCCACGGCGCTCAGCTTGGGCACTTCTGACCCCGATGCGCTG	1380
Db	1373	GTGCGCTTGTCAATTTCCACGGCGCTCAGCTTGGGCACTTCTGACCCCGATGCGCTG	1432
QY	1381	GCCCACTTCAACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACTTTTGAACAGGCG	1440
Db	1433	GCCCACTTCAACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACTTTTGAACAGGCG	1492
QY	1441	TCCCAACGCGCAGGCAACAAAGCCCAAGCCCTTAAAGGGGGAAGCTGCGAGCTCCGCGCC	1500
Db	1493	TCCCAACGCGCAGGCAACAAAGCCCAAGCCCTTAAAGGGGGAAGCTGCGAGCTCCGCGCC	1552
QY	1501	CTTGAACGTGGGAGCATGTGCTGAGAGATGCTGTGGGGAAGATGTGCGCGCCGAGTACCC	1560
Db	1553	CTTGAACGTGGGAGCATGTGCTGAGAGATGCTGTGGGGAAGATGTGCGCGCCGAGTACCC	1612
QY	1561	TTCGGGGGGCCCTTGGGACCTTCAACCCAGGCAAGGCTTTCGGGGGAAGCATGTATCTGCTC	1620
Db	1613	TTCGGGGGGCCCTTGGGACCTTCAACCCAGGCAAGGCTTTCGGGGGAAGCATGTATCTGCTC	1672
QY	1621	TTCGGAACAAGCCACCTTGCGCGCTCTCGCTGATGTGAGCTCGGGCAGGCGCCCTTGAGC	1680
Db	1673	TTCGGAACAAGCCACCTTGCGCGCTCTCGCTGATGTGAGCTCGGGCAGGCGCCCTTGAGC	1732
QY	1681	GACCTGCTCTTTTGGGCACTGTTGTGAACAGGGCAACAGTGCATGTATCTTGGGAG	1740
Db	1733	GACCTGCTCTTTTGGGCACTGTTGTGAACAGGGCAACAGTGCATGTATCTTGGGAG	1792

Query Match	67.9%	Score 2758;	DB 11;	Length 3118;
Best Local Similarity	88.5%	Pred. No. 0;		
Matches 2758; Conservative	0;	Mismatches 360;	Indels 0;	Gaps 0;

QY	595	ATGGCCAGACATCTGGGGGACCAAGTGGTGGCCATGGGTGTGGCCCTCTGGGGGTGGGTG	654
Db	1	ATGGCCAGACATCTGGGGGACCAAGTGGTGGCCATGGGTGTGGCCCTCTGGGGGTGGGTG	60
QY	655	CGAATATAGACAACCTCATCAACCCCAAGGGCTGTTCCCTGCGAGGTAACGGGTGGGC	714
Db	61	CGAATATAGACAACCTCATCAACCCCAAGGGCTGTTCCCTGCGAGGTAACGGGTGGGC	120
QY	715	GGTAGCCCGAGAGACGGGGTCCAGTTTCCCTGGACTACAACTACCTCGGCTTCTTCCTG	774
Db	121	GGTAGCCCGAGAGACGGGGTCCAGTTTCCCTGGACTACAACTACCTCGGCTTCTTCCTG	180
QY	775	GTGAGCAGCGGCACACACGGCTGCTGGGGGGCGGAACCGCTTCCCTTGGCTCTGGAG	834
Db	181	GTGAGCAGCGGCACACACGGCTGCTGGGGGGCGGAACCGCTTCCCTTGGCTCTGGAG	240
QY	835	TCCTACATCTACACAGCAGAGACGGGCGTGGGAGGGACCTGGAAATTGACATCCCTGCTG	894
Db	241	TCCTACATCTACACAGCAGAGACGGGCGTGGGAGGGACCTGGAAATTGACATCCCTGCTG	300
QY	895	CTCTCTCATATTGATGATGAGAAATGTTGACGCCAATTAGAACGCCACCCAGGCT	954
Db	301	CTCTCTCATATTGATGATGAGAAATGTTGACGCCAATTAGAACGCCACCCAGGCT	360
QY	955	CAGCTCCCATGTCTCTCTGGCTGGCTCAGGGGGAGCTGGGGATCTGCTTGGCGGAGAC	1014
Db	361	CAGCTCCCATGTCTCTCTGGCTGGCTCAGGGGGAGCTGGGGATCTGCTTGGCGGAGAC	420
QY	1015	CTGGAAGACACTGAGGCCCCAGAGGAGTGGGGAGCCAGGACAAAGGGAGACCCGACATGCA	1074
Db	421	CTGGAAGACACTGAGGCCCCAGAGGAGTGGGGAGCCAGGACAAAGGGAGACCCGACATGCA	480
QY	1075	ATCAGGCGTTCCTTCCCAAAGGGGACCTTGAGTCTTGAGGCCAGGTGAGAGATT	1134
Db	481	ATCAGGCGTTCCTTCCCAAAGGGGACCTTGAGTCTTGAGGCCAGGTGAGAGATT	540
QY	1135	ATGATCCGGGAAGAGCTCTCTGACAGTCTATTCCTTGAGGATGGGTCTGAGGAATTCCAG	1194
Db	541	ATGATCCGGGAAGAGCTCTCTGACAGTCTATTCCTTGAGGATGGGTCTGAGGAATTCCAG	600
QY	1195	ACCAATGATTTGAAGAGCCCTTGTAAGAGCTGTGGGAGCTCGAGAGGCTCAGCCTACCTG	1254
Db	601	ACCAATGATTTGAAGAGCCCTTGTAAGAGCTGTGGGAGCTCGAGAGGCTCAGCCTACCTG	660
QY	1255	GATGAGCTGCGTTTGGCTGTGGCTTGAACCGCGTGAACATTGCCAGAGTGAACCTCTT	1314
Db	661	GATGAGCTGCGTTTGGCTGTGGCTTGAACCGCGTGAACATTGCCAGAGTGAACCTCTT	720
QY	1315	CGGGGGGACATCCAAATGGCGGTCTTCCATCTCGAAGCTTCCCTATATGAAGCCCTGCTG	1374
Db	721	CGGGGGGACATCCAAATGGCGGTCTTCCATCTCGAAGCTTCCCTATATGAAGCCCTGCTG	780
QY	1375	AATGACCGGCGTGAAGTTCGTGCGCTTGCTCAATTTCCACCGGCTCAGCTGGGACCATTC	1434
Db	781	AATGACCGGCGTGAAGTTCGTGCGCTTGCTCAATTTCCACCGGCTCAGCTGGGACCATTC	840
QY	1435	CTGACCCCGATGCGCTGAGCCCACTCTACAGCGGCGGCGCTTCCAACTGCTCATCCGC	1494
Db	841	CTGACCCCGATGCGCTGAGCCCACTCTACAGCGGCGGCGCTTCCAACTGCTCATCCGC	900
QY	1495	AACTTTTGGACACAGGCGTCCACAGCGCCAGGACCAAGAACGCCACCTTAAAGGGGGA	1554
Db	901	AACTTTTGGACACAGGCGTCCACAGCGCCAGGACCAAGAACGCCACCTTAAAGGGGGA	960
QY	1555	GCTGCGAGACTCCGGCCCTCTGACCTGGGAGCATGTCTGAGGATGCTCTGTGGGAAAGATG	1614
Db	961	GCTGCGAGACTCCGGCCCTCTGACCTGGGAGCATGTCTGAGGATGCTCTGTGGGAAAGATG	1020
QY	1615	TGCGCGCGGAGTACCTCTCGGGGGCGCTTGGACCTTCAACCCAGGCAAGGCTTTCGGG	1674
Db	1021	TGCGCGCGGAGTACCTCTCGGGGGCGCTTGGACCTTCAACCCAGGCAAGGCTTTCGGG	1080

QY	1675	GAGAGCATGTATCTGCTCTCGGACAAAGGCACCTCGCGGCTCTCGGTGGATAGTGGGCTTC	1734
Db	1081	GAGAGCATGTATCTGCTCTCGGACAAAGGCACCTCGCGCTCTCGGTGGATGTGGGCTTC	1140
QY	1735	GAGCAGAGCCCTCGTAGAGCAGCTGCTTCTTTTGGGCACTGTGCTGAAACAAGGCACAGATG	1794
Db	1141	GAGCAGAGCCCTCGTAGAGCAGCTGCTTCTTTTGGGCACTGTGCTGAAACAAGGCACAGATG	1200
QY	1795	GCCATGTACTTCTGGGAGATGGGTTCCAAATGCATTTTCTCAGCTCTTGGGGCTGTGTTG	1854
Db	1201	GCCATGTACTTCTGGGAGATGGGTTCCAAATGCATTTTCTCAGCTCTTGGGGCTGTGTTG	1260
QY	1855	CTGCTCCGGGTGATATGGCAACGCTGGAGGCTTGAACGCTGAGAGAGGACAGAGAGAAAGAC	1914
Db	1261	CTGCTCCGGGTGATATGGCAACGCTGGAGGCTTGAACGCTGAGAGAGGACAGAGAGAAAGAC	1320
QY	1915	CTGGCGTTCAAGTTTGAGGGAGATGGAGCGTTGACCTTTTGGCGAGTGTATCGCACAGT	1974
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QY	1975	GAGGTGAGGGCTGCCGCTCTCTCGTCCGTCCGTCGCGGCTCTGGGGGAGATGCACTTGC	2034
Db	1381	GAGGTGAGGGCTGCCGCTCTCTCGTCCGTCCGTCGCGGCTCTGGGGGAGATGCACTTGC	1440
QY	2035	CTCCAGCTGGCCATGCAATGCAATGACGCCCGGTGCTTTTGGCCAGATGGGGTACAGTCT	2094
Db	1441	CTCCAGCTGGCCATGCAATGCAATGACGCCCGGTGCTTTTGGCCAGATGGGGTACAGTCT	1500
QY	2095	CTGCTGACACAGAAATGGTGGGGAGATATATGGCAGACACTACACCATCTGGGCCCTGATT	2154
Db	1501	CTGCTGACACAGAAATGGTGGGGAGATATATGGCAGACACTACACCATCTGGGCCCTGATT	1560
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Db	1561	CTCGGCTTCTTTTGGCCTTCCACTCATCTACACCCGCTCATCACTTCAGAAATCAGAA	1620
QY	2215	GAGAGGCCCAACACGGGAGAGCTTAAGTTTGACATGATATGTCTATTATGGGGAAAGG	2274
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QY	2275	CGTGCAGGAGCGAGCGAGACCGACGCGAGAAAGACGCGCTGGGGGTCCCGGCGCCAGTGGGC	2334
Db	1681	CGTGCAGGAGCGAGCGAGACCGACGCGAGAAAGACGCGCTGGGGGTCCCGGCGCCAGTGGGC	1740
QY	2335	CGTCCGGGTTGTGCGGGGGGCGCTGCGGGGGGCGCGGTGCTACAGCCGCTGGTTCCAC	2394
Db	1741	CGTCCGGGTTGTGCGGGGGGCGCTGCGGGGGGCGCGGTGCTACAGCCGCTGGTTCCAC	1800
QY	2395	TTCTTGGGCGCGCGGTGACCATCTTTCATGAGGCAACGTGTGACACTGCTGTTTCTTG	2454
Db	1801	TTCTTGGGCGCGCGGTGACCATCTTTCATGAGGCAACGTGTGACACTGCTGTTTCTTG	1860
QY	2455	CTGCTTTTCTGCGGGGTGTGCTGTGAGATTTCAGCGGGCGCGCGCGGCTCGTAGAG	2514
Db	1861	CTGCTTTTCTGCGGGGTGTGCTGTGAGATTTCAGCGGGCGCGCGCGGCTCGTAGAG	1920
QY	2515	CTGCTGCTCTATTTTCTGGGCTTTTCAAGCTGTGCTGTGAGAACTGCGCCAGGCTGAGC	2574
Db	1921	CTGCTGCTCTATTTTCTGGGCTTTTCAAGCTGTGCTGTGAGAACTGCGCCAGGCTGAGC	1980
QY	2575	GAGAGCGGGGAGCACTGTCGACAGCGGGGGGCCCCGGGCTGGCCATGCTTACAGCCAG	2634
Db	1981	GAGAGCGGGGAGCACTGTCGACAGCGGGGGGCCCCGGGCTGGCCATGCTTACAGCCAG	2040
QY	2635	CGCCGTGGCCCTTACTGTCGCGGACAGCTGGAACAGATGAGCCTTAATGTGCTTCACTGCG	2694
Db	2041	CGCCGTGGCCCTTACTGTCGCGGACAGCTGGAACAGATGAGCCTTAATGTGCTTCACTGCG	2100
QY	2695	TTCTCTCTGAGGAGTGGAGCTGCGGCTGACCCGAGGTTTGTACACACTGGGCCGACATGTC	2754
Db	2101	TTCTCTCTGAGGAGTGGAGCTGCGGAGGTTTTTCAAGGTGGGCTTTCACATCTTCAAGGTCAACAA	2160
QY	2755	CTTGCATGCACTTATGAGTTTTTCAAGGTGGGCTTTCACATCTTCAAGGTCAACAA	2814

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 08:59:09 ; Search time 651 Seconds
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11088.599 Million cell updates/sec

Title: US-09-869-486B-29

Perfect score: 4061
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1505	37.1	1524	US-09-020-956-109	Sequence 109, App
2	1505	37.1	1524	US-09-030-607-109	Sequence 109, App
3	1505	37.1	1524	US-09-439-313-109	Sequence 109, App
4	1505	37.1	1524	US-09-352-616A-109	Sequence 109, App
5	1505	37.1	1524	US-09-232-149A-109	Sequence 109, App
6	1505	37.1	1524	US-09-159-812-109	Sequence 109, App
7	1505	37.1	1524	US-09-636-215-109	Sequence 109, App
8	1505	37.1	1524	US-09-685-166A-109	Sequence 109, App
9	1505	37.1	1524	US-09-115-453-109	Sequence 109, App
10	1505	37.1	1524	US-09-688-489-109	Sequence 109, App
11	1505	37.1	1524	US-09-759-142-109	Sequence 109, App
12	1505	37.1	1524	US-09-651-236-109	Sequence 109, App
13	1505	37.1	1524	US-09-651-236-109	Sequence 109, App
14	1505	37.1	1524	US-09-030-606-109	Sequence 109, App
15	1505	37.1	1524	US-09-657-279-109	Sequence 109, App
16	1505	37.1	1524	US-10-012-896-109	Sequence 109, App
17	1230.2	30.3	1297	US-08-727-688-9	Sequence 109, App
18	815.8	20.1	3498	US-09-949-016-1003	Sequence 1003, App
19	814.2	20.0	3498	US-09-020-956-8	Sequence 5521, App
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21	446.8	11.0	799	US-09-439-313-8	Sequence 8, Appli
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23	446.8	11.0	799	US-09-232-149A-8	Sequence 8, Appli
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25	446.8	11.0	799	3	US-09-159-812-8	Sequence 8, Appli
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27	446.8	11.0	799	3	US-09-685-166A-8	Sequence 8, Appli
28	446.8	11.0	799	3	US-09-115-453-8	Sequence 8, Appli
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30	446.8	11.0	799	3	US-09-679-426-8	Sequence 8, Appli
31	446.8	11.0	799	3	US-09-759-143-8	Sequence 8, Appli
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34	446.8	11.0	799	3	US-09-657-279-8	Sequence 8, Appli
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36	429.6	10.6	6220	3	US-09-600-087-1	Sequence 470, App
37	429.6	10.6	6220	3	US-09-949-016-470	Sequence 5229, App
38	428	10.5	6221	3	US-09-020-956-9	Sequence 9, Appli
39	395.8	9.7	801	3	US-09-030-607-9	Sequence 9, Appli
40	395.8	9.7	801	3	US-09-439-313-9	Sequence 9, Appli
41	395.8	9.7	801	3	US-09-352-616A-9	Sequence 9, Appli
42	395.8	9.7	801	3	US-09-232-149A-9	Sequence 9, Appli
43	395.8	9.7	801	3	US-09-159-812-9	Sequence 9, Appli
44	395.8	9.7	801	3	US-09-636-215-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-020-956-109
Sequence 109, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-109
Query Match 37.1%; Score 1505; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 CTGCGCCAGAGGCTGAGCGAGAGCGAGGCGAGAGGCTGCGCAGCGAGGAGCGCGGCGCTTGGC 2616
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QY 2617 CATGCTCACTGAGGCGAGCGCTGCGCTCTACCTGCGCGAGCAGCTGGAGCAAGTGGAGC 2676
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QY 2677 CTAGTGGCTCACTGAGGCTGCTTCTGAGGCGTGGAGCGTGGAGCGGCTGAGCCCGGATTGGAC 2736
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QY 2797 ATCTTCACGCTCAACAACAGCTGGGCGCCAAAGATGCTCATGTAAGCAAGTATGAAG 2856
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QY 2857 GACGCTTTCTTCTTCTTCTTCTTCTGCGCGTGGAGCTGATGAGCCTATGGCGGCGACG 2916
Db 310 GACGCTTTCTTCTTCTTCTTCTTCTGCGCGTGGAGCTGATGAGCCTATGGCGGCGACG 369
QY 2917 GAGGCGCTCTGAGGCGGCGGAGCAGTGAATTTCCCAATATCTGCGCGGCTTCTTAC 2976
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QY 2977 CGTCCCTACCTGAGATCTTGGGAGATTTCCCGAGAGGACATGGAAGTGGCGCTCATG 3036
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QY 3157 CTGCTGGGCAACATCTGCTGATCTTGGCATTTGCGATTCAGTTACATTCGCG 3216
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QY 3397 TTCCGGGTTTACCTTTTAAAGAAAGCGAGCGGAACTGCTTAAAGTGGAAATCGTGAT 3456
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Db 1270 TTGAGTGAAGCCCATATGATCATCTGGGCGCACTGTCAGAGCACCTTTGGAGTGCATCC 1329
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Db 1330 TTCAACAACAGAGATCCCGGCTCTCTCCAGAAACAGATCCCACTGGAGATCAAG 1389
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Db 1390 CTGATATCCGGGCGCTTATTCATCTGAGAGCTGCAAGGCTTGGGATTAACAGGACA 1449
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QY 4057 AAAA 4061
Db 1510 AAAA 1514

RESULT 2
US-09-607-109
; Sequence 109, Application us/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEO ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 08:59:09 ; Search time 2245 Seconds
(without alignment)
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Title: US-09-869-486B-29

Perfect score: 4061
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333234308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: genebegn2003ds:*
12: genebegn2004as:*
13: genebegn2004bs:*
14: genebegn2005as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4061	100.0	4061	3	AAA49923 Human cal
2	4061	100.0	4061	10	ADH62711 Ca activa
3	4061	100.0	4061	13	ADR73511 Human TRP
4	4061	100.0	4061	13	ADSI2774 Transient
5	4061	100.0	4061	14	ADV97224 Human cat
6	4028.4	99.2	4002	6	ADJ32372 Human Trp
7	4001	98.5	4001	14	ACL38958 TRPM4 cod
8	3845	97.7	4641	11	ADN39239 Cancer/an
9	3812.2	97.9	3898	12	ADL06463 Human tum
10	3758.6	92.6	3810	6	ABK92167 Prostate
11	3759.6	92.6	3810	13	ADR66772 Human pro
12	3759.6	92.6	3810	13	ADR66772 Human pro
13	3759.6	92.6	3810	13	ADSI2778 Human TRP
14	3721.4	91.6	3900	5	AAH76383 Human TRP
15	3721.4	91.6	3900	8	ABSS8041 Human tra
16	3721.4	91.6	3900	12	ADH51622 Human 186
17	3579.8	88.2	3599	6	ABK28677 Human CDN
18	3542	87.2	3701	13	ADSI2776 Transient
19	3538.8	87.1	3676	12	ADQ83682 Human tum

20	3538.8	87.1	3676	13	ADQ85834	Adq85834 Human tum
21	3538.8	87.1	3676	13	ADQ86998	Adq86998 Human tum
22	3501	86.2	3501	6	ABK92224	Abk92224 Prostate
23	3501	86.2	3501	11	ADN39597	Adn39597 Cancer/an
24	3399	83.7	3583	11	ADL33391	Adl33391 Human tra
25	3376.8	83.2	3390	12	ADH51624	Adh51624 Human 186
26	3373.8	83.1	3387	5	AAH76384	Aah76384 Human TRP
27	2616.4	64.4	2695	6	AAH76384	Aah76384 Human TRP
28	2412.4	59.4	2459	12	ADL06424	Adl06424 Human tum
29	2258	55.6	2393	2	ADL06424	Adl06424 Human tum
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31	1978.8	48.7	2180	3	AAH49921	Aah49921 Human cal
32	1505	37.1	1524	2	AAV58585	Aav58585 Prostate
33	1505	37.1	1524	2	AAV61200	Aav61200 Full leng
34	1505	37.1	1524	3	AAH06348	Aah06348 Human tum
35	1505	37.1	1524	3	ABK71253	Abk71253 Human pro
36	1505	37.1	1524	4	AAH93464	Aah93464 Human pro
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38	1505	37.1	1524	4	AAH02529	Aah02529 Prostate
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40	1505	37.1	1524	5	ACA59365	Aca59365 Prostate
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42	1505	37.1	1524	6	ABU94528	Abu94528 Human J1-
43	1505	37.1	1524	6	ABSS8637	Abss8637 Prostate
44	1505	37.1	1524	8	ACC95092	Acc95092 Prostate
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ALIGNMENTS

RESULT 1
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AC
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DT 10-OCT-2000 (first entry)
XX
DE Human calcium channel SOC-3/CRAC-2 cDNA.
XX
XX SOC-2/CRAC-1; calcium channel; human; store operated channel;
KW calcium release activated channel; therapy; diagnosis;
KW lymphocyte proliferative disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 382..5979
FT P-PSDB; AA95436.
XX
XX W0200040614-A2.
XX
XX PD 13-JUL-2000.
XX PF 20-DEC-1999; 99WO-US029996.
XX PR 30-DEC-1998; 98US-0114220P.
XX PR 29-JAN-1999; 99US-0120018P.
XX PR 22-JUN-1999; 99US-0140415P.
XX
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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XX Schatzberg AM;
XX WPI; 2000-465957/40.
XX P-PSDB; AA95436.
XX
XX New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT diagnose and treat proliferative disorders associated with the channel,
PT and to screen for novel modulators of the channel.
XX
XX Claim 1(a); Page 99-100; 108pp; English.


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Location/Qualifiers
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GenCore version 5.1.6
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Run on: January 6, 2006, 08:58:55 ; Search time 8833 Seconds
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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
filtering filter 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	770	35.3	912	6 CA488162	CA488162 AGENCOURT
5	719	33.0	879	5 BU858032	BU858032 AGENCOURT
6	651.6	22.9	883	5 BQ723742	BQ723742 AGENCOURT
7	647	22.7	864	6 CA488844	CA488844 AGENCOURT
8	644.4	22.6	862	7 CQ031569	CQ031569 AGENCOURT
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10	609.8	26.5	599	3 BI910079	BI910079 603067915
11	579.8	26.5	580	3 BP265210	BP265210 BP265210
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15	525.6	24.1	551	6 CB266373	CB266373 1005278 H
16	514.4	23.6	1090	2 BF311909	BF311909 601897749
17	499.2	22.9	540	7 CN335029	CN335029 170004277
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19	485.4	22.3	625	2 BI199159	BI199159 602758878
20	483	22.2	483	3 BQ084154	BQ084154 K-EST0148
21	478	21.9	698	8 DN935712	DN935712 AGENCOURT
22	465.6	21.4	3449	4 AK035197	AK035197 Mus muscu

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24	463.2	21.2	997	2 BF310664	BF310664 601894621
25	459.2	21.1	751	7 CQ031892	CQ031892 CQ031892
26	451	20.7	933	5 BQ942718	BQ942718 AGENCOURT
27	449.2	20.6	3523	4 AK044423	AK044423 Mus muscu
28	447.4	20.5	624	7 CK832049	CK832049 4056009 B
29	443	20.3	444	3 BM821224	BM821224 K-EST0090
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31	395	18.1	519	2 BI198633	BI198633 602761709
32	391.2	17.9	392	3 BM797899	BM797899 K-EST0081
33	389	17.8	569	7 CN677997	CN677997 E0104H02
34	387.6	17.8	611	2 BE313619	BE313619 601153249
35	387.2	17.6	869	7 CK942304	CK942304 4065798 B
36	382.8	17.6	869	3 BI488582	BI488582 603021110
37	379.6	17.4	444	1 AM816479	AM816479 QVO-ST023
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ALIGNMENTS

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DEFINITION DQ031081.1 GI:66882285
ACCESSION DQ031081
VERSION DQ031081.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 3118)
Nilsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeille,D.,
White,T.J., Snielsky,J.J., Adams,M.D. and Cargill,M.
White,T.J., Snielsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
Chimpanzees
(ex) PLOS Biol. 3 (6), E170 (2005)
JOURNAL PUBMED 15869325
2 (bases 1 to 3118)
Nilsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeille,D.,
White,T.J., Snielsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Best Local Similarity 81.7%; Pred. No. 0;
Matches 1559; Conservative 1; Mismatches 349; Indels 0; Gaps 0;

[illegible][illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 08:58:54 ; Search time 410 Seconds
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9451.425 Million cell updates/sec

Title: US-09-869-486B-25

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing larger 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	1149.8	52.7	1524	US-09-232-149A-109	Sequence 109, App
6	1149.8	52.7	1524	US-09-159-813-109	Sequence 109, App
7	1149.8	52.7	1524	US-09-636-215-109	Sequence 109, App
8	1149.8	52.7	1524	US-09-685-166A-109	Sequence 109, App
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14	1149.8	52.7	1524	US-09-030-606-109	Sequence 109, App
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18	538.6	24.7	3498	US-09-949-016-1003	Sequence 9, Appl
19	535.4	24.6	3498	US-09-949-016-5521	Sequence 1003, Ap
20	358	16.4	384	US-09-030-607-185	Sequence 185, App
21	358	16.4	384	US-09-439-313-185	Sequence 185, App
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39	348.6	16.0	380	US-09-232-149A-84	Sequence 84, Appl
40	348.6	16.0	380	US-09-159-812-84	Sequence 84, Appl
41	348.6	16.0	380	US-09-636-215-84	Sequence 84, Appl
42	348.6	16.0	380	US-09-685-166A-84	Sequence 84, Appl
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44	348.6	16.0	380	US-09-688-489-84	Sequence 84, Appl
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ALIGNMENTS

RESULT 1
US-09-020-956-109
Sequence 109, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillian, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-109
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Best Local Similarity 88.6%; Pred. No. 66-245;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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DB 1030 GAACAGCGCTTAAAGTCTGAGCGGAGGAGTTCAGAGTGAAGCGGCTGCGGAGTGA 1089
QY 1916 ----- 1915

DB 1090 GTGGCGAGGCGCTGAGCGGCTGCTGCTTGTGCCCCAGGTGGGCGGCAACCCCTGAC 1149
QY 1916 ----- 1915
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DB 1210 ATTTTCTCTAGATGTAAGCTCATCTGAGGCTTGGGCGGCGGCACTGTGGGCTTGTTC 1269
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DB 1270 TTGAGTGAAGCCCATGCTGATGAGGCGCACTGTGAGGACCACTTTGGAGTGCATCC 1329
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DB 1330 TTACAAACACAGAGATCCCGGCTCTCCGAGAACAGTCCAGGCTGGAGATCAAG 1389
QY 2066 CTGAGATCCCGGCGGTTATCATCTGAGGCTGAGGCTCTTGGGCTAACAGGACCA 2125
DB 1390 CTGAGATCCCGGCGGTTATCATCTGAGGCTGAGGCTCTTGGGCTAACAGGACCA 1449
QY 2126 CAGACCCCTGACACATGATTCCTGACATGGGGGAATTAAGCATTTACAG 2180
DB 1450 CAGACCCCTGACACATGATTCCTGACATGGGGGAATTAAGCATTTACAG 1504

RESULT 2
US-09-030-607-109
Sequence 109, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-109
Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 6e-245;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 08:58:52 ; Search time 1330 Seconds
(without alignment)
10924.083 Million cell updates/sec

Title: US-09-869-486B-25
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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10: geneseqn20038: *
11: geneseqn20038: *
12: geneseqn20048: *
13: geneseqn20048: *
14: geneseqn20058: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	1978.8	90.8	3900	5	AAH76383 Human tra
7	1978.8	90.8	3900	8	ABSS58041 Human tra
8	1978.8	90.8	3900	12	ADH51622 Human 186
9	1978.8	90.8	4001	14	ACL38958 TRPM4 cod
10	1978.8	90.8	4061	3	AAA49923 Human cal
11	1978.8	90.8	4061	10	ADH62711 Ca activa
12	1978.8	90.8	4061	13	ADR73511 Human TRP
13	1978.8	90.8	4061	13	ADSL2774 Transient
14	1978.8	90.8	4061	14	ADV97224 Human cat
15	1978.8	90.8	4641	11	ADN39239 Cancer/an
16	1977.2	90.7	2695	6	AAJ32373 Human Trp
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19	1975.6	90.6	3810	13	ADR66772 Human pro

20	1975.6	90.6	3810	13	ADR65869	Adt65869 Human pro
21	1975.6	90.6	3810	13	ADSL2778	Adt12778 Human TRP
22	1975.6	90.6	3898	12	ADL06463	Adt06463 Human tum
23	1974.8	90.6	3701	13	ADSL2776	Adt12776 Transient
24	1968.2	90.3	3599	6	ABK28677	ABK28677 Human CDN
25	1943.8	89.2	2459	12	ADL06424	Adt06424 Human tum
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27	1892.2	86.8	3390	12	ADH51624	Adh51624 Human 186
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35	1149.8	52.7	1524	3	AAH06348	AAH06348 Human imm
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39	1149.8	52.7	1524	4	AAH02529	AAH02529 Prostate
40	1149.8	52.7	1524	4	AAH84778	AAH84778 Human pro
41	1149.8	52.7	1524	5	ACA59365	ACA59365 Prostate
42	1149.8	52.7	1524	5	AAH10107	AAH10107 Human pro
43	1149.8	52.7	1524	6	ABL94928	ABL94928 Human J1-
44	1149.8	52.7	1524	6	ABH58637	ABH58637 Prostate
45	1149.8	52.7	1524	8	ACC95092	ACC95092 Prostate

ALIGNMENTS

RESULT 1	AAA49921	standard; cDNA; 2180 BP.
ID	AAA49921	
AC	AAA49921;	
XX		
XX		
DT	10-OCT-2000	(first entry)
XX		
DE	Human calcium channel SOC-3/CRA-2 partial cDNA.	
XX		
XX	SOC-3/CRA-2; calcium channel; human; store operated channel;	
KW	calcium release activated channel; therapy; diagnosis;	
KW	lymphocyte proliferative disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..2180
FT		/*tag= a
FT		/partial
XX		
XX	WO200040614-A2.	
PN		
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PD	13-JUL-2000.	
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PF	20-DEC-1999;	99WO-US029996.
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PR	30-DEC-1998;	98US-0114220P.
PR	29-JAN-1999;	99US-0120018P.
PR	22-JUN-1999;	99US-0140415P.
XX		
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.	
XX		
PI	Scharenberg AM;	
XX		
DR	WPI; 2000-465957/40.	
XX		
DR	P-PSDB; AA95434.	
XX		
PT	New SOC/CRA-2 calcium channel polynucleotides and polypeptides used to	
PT	diagnose and treat proliferative disorders associated with the channel,	
PT	and to screen for novel modulators of the channel.	
XX		

PS Claim 1(a); Page 90-91; 108bp; English.

XX The present sequence is a partial nucleotide sequence of human SOC-3/CRAC
CC -2 cDNA. A partial open reading frame encodes the C-terminal portion (see
CC AY95134) of SOC-3/CRAC-2, a member of a novel family of store operated
CC channel (SOC) or calcium release activated channel (CRAC) polypeptides
CC that modulate Ca²⁺ flux into and out of a cell, and which may be
CC activated upon depletion of Ca²⁺ from intracellular calcium stores,
CC allowing Ca²⁺ influx into a cell. SOC-3/CRAC-2 (full-length cDNA given in
CC AA49923) is expressed predominantly in the kidney and colon.

CC Compositions for expressing SOC/CRAC calcium channel polypeptides in
CC cells may be useful for treating patients that have reduced extracellular
CC calcium influx into their SOC/CRAC-expressing cells. They will also be
CC useful for delivering therapeutic and/or imaging agents to such cells to
CC modulate proliferation and growth. SOC/CRAC polypeptides also represent
CC targets for designing and/or identifying inhibitors that block lymphocyte
CC proliferation and binding agents that selectively bind to SOC/CRAC
CC polypeptides to which drugs or toxins can be conjugated for delivery to
CC SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used as probes
CC and primers to identify other members of the SOC/CRAC family of calcium
CC channels, as diagnostic reagents for identifying the presence of SOC/CRAC
CC polypeptides in biological samples, as agents for generating SOC/CRAC
CC binding polypeptides, and in gene therapy. Methods for determining the
CC level of SOC/CRAC expression in a subject can be used to assess the
CC presence, or absence, or stage of a proliferative disorder, e.g. a
CC lymphocyte proliferative disorder

XX Sequence 2180 BP; 365 A; 694 C; 667 G; 451 T; 0 U; 3 Other;

Query Match 99.9%; Score 2178.8; DB 3; Length 2180;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TGGGCACTGTTGCTGAACAGGACAGAGTGGCCATGACTTCTGGAGATGGTTCCAT 120
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QY 181 GACCTGTGAGAGGACAGCAGAGGAAAGACTGCGCTTCAAGTTTGAAGGGATGGCGCT 240
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DB 301 CGCTGCCCGCTCTGGGGGGAGTGCATCTTCCAGCTGCGCAGTGAAGCTGAGCGCCGT 360
QY 361 GCTTCTTTGGCCAGATGGGGTACAGTCTCTGTCGACACAGAACTGGTGGGAGATATG 420
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QY 421 GCCAGCACTACACCATCTGGGCTCTGCTTCTGCTTTTGGCTTCCATCTAC 480
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QY 481 ACCGGCTCACTACCTTACAGAAATCAGAAAGAGCCCAACAGGAGAGACTTGAAGTT 540
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QY 541 GACATGATATGTATTAATGGGAGAGGCTGCGGAGCGGAGACCCAGCGAGAG 600
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QY 601 ACGCGCTGAGGATCCCGCGCACTGCGGCTCGGATGCTGCGGAGCGCTGCGG 660
DB 601 ACGCGCTGAGGATCCCGCGCACTGCGGCTCGGATGCTGCGGAGCGCTGCGG 660
QY 661 GGGGGCGGAGGCTTACGCGCGCTGCTTCACTTCTGGGGCGCGGAGACATCTTATG 720
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 08:58:54 ; Search time 1162 Seconds
(without alignments)
1101.839 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1977.2	90.7	2695	AX443325	Sequence
7	1977.2	90.7	4042	AX443327	Sequence
8	1975.6	90.6	3810	CO896241	Sequence
9	1975.6	90.6	3810	AK000048	Homo sapi
10	1974.4	90.6	3701	AY046396	Homo sapi
11	1968.2	90.3	3599	AX402516	Sequence
12	1892.2	86.8	3387	AX235185	Sequence
13	1892.2	86.8	3402	CO715325	Sequence
14	1892.2	86.8	3523	AY297044	Homo sapi
15	1892.2	86.8	3879	AY297045	Homo sapi
16	1891	86.7	3393	BD082082	Reagent
17	1793.8	82.3	2981	AK000235	Homo sapi
18	1196	54.9	2737	BC046472	Mus muscu

19	1196	54.9	2993	9	BC058632
20	1196	54.9	4000	9	MMU575814
21	1196	54.9	4053	9	BC096475
22	1194.4	54.8	3725	9	BC049165
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26	1149.8	52.7	1524	6	BD242021
27	1149.8	52.7	1524	6	AR237204
28	1149.8	52.7	1524	6	AR237828
29	1149.8	52.7	1524	6	AR366524
30	1149.8	52.7	1524	6	AR370820
31	1149.8	52.7	1524	6	AR392325
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33	1149.8	52.7	1524	6	AR405227
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD270154 2180 bp DNA linear PAT 17-JUL-2003
BD270154
BD270154.1 GI:33079922
JP 2002536966-A/13.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 2180)
Scharenberg, A.M.
Characterization of a calcium channel family
Patent: JP 2002536966-A 13 05-NOV-2002;
BETH ISRAEL DEACONESS MEDICAL CENTER INC
OS Homo sapiens (human)
PN JP 2002536966-A/13
PD 05-NOV-2002
PF 20-DEC-1999 JP 2000592322
PR 30-DEC-1998 US 60/144220, 29-JAN-1999 US 60/120018 PR
22-JUN-1999 US 60/140415
PI ANDREW M. SCHARENBERG
PC C12N15/09, A61K31/7115, A61K31/712, A61K31/7125, A61K35/76, A61K38/
PC 00/
PC A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P3/14, A61P43/00,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/48, C12Q1/
PC 68, G01N33/15,
PC G01N33/50, G01N33/53, G01N33/56, G01N33/577, C12N15/00, C12N5/00,
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FT location/Qualifiers
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FEATURES

source
location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 901 CCGGGGCTTGCCATGCTCACTAGGCGAGCGCTCTTCACTTCCGCGAGAGCTGG 960
DB 901 CCGGGGCTTGCCATGCTCACTAGGCGAGCGCTCTTCACTTCCGCGAGAGCTGG 960
QY 961 AACCAATGCGAATGAGGCTTCAACCTGTTCCCTGGGCGTGGGCTGGCGCTGAGC 1020
DB 961 AACCAATGCGAATGAGGCTTCAACCTGTTCCCTGGGCGTGGGCTGGCGCTGAGC 1020

QY 1021 CCGGGTTTGTACCACTTGGGCGGCACTGTCTCTGATGCACTTCAATGTTTTCAGGTTG 1080
DB 1021 CCGGGTTTGTACCACTTGGGCGGCACTGTCTCTGATGCACTTCAATGTTTTCAGGTTG 1080
QY 1081 CCGGTGCTTCACTTTCACAGGTCAACAAACAGCTGGGGGCCAAAGATCTCATGTGAGC 1140
DB 1081 CCGGTGCTTCACTTTCACAGGTCAACAAACAGCTGGGGGCCAAAGATCTCATGTGAGC 1140
QY 1141 AAGATGATGAAGACGATGTTCTTCTCTCTCTCTGCGGCTGGTGGTGAAGCTAT 1200
DB 1141 AAGATGATGAAGACGATGTTCTTCTCTCTCTCTCTCTGCGGCTGGTGGTGAAGCTAT 1200
QY 1201 GCGGTGCAACGAGAGGGCTCTGAGGCAAGGACAGTACATTTCCCAATATCTGCGC 1260
DB 1201 GCGGTGCAACGAGAGGGCTCTGAGGCAAGGACAGTACATTTCCCAATATCTGCGC 1260
QY 1261 CGGCTCTTCAACGCTCCCTACCTGACAGATCTTGGGCAATTTCCCAAGAGACATGAGC 1320
DB 1261 CGGCTCTTCAACGCTCCCTACCTGACAGATCTTGGGCAATTTCCCAAGAGACATGAGC 1320
QY 1321 GTGGCCTCATGAGACACAGCAATGCTGCTGCGAGGCGGCTTCTGGGCAACCTCTCT 1380
DB 1321 GTGGCCTCATGAGACACAGCAATGCTGCTGCGAGGCGGCTTCTGGGCAACCTCTCT 1380
QY 1381 GGGGCCAGGCGGACCTGCTGCTCCAGTATGCAATGCGTGGTGGTGTGCTCTC 1440
DB 1381 GGGGCCAGGCGGACCTGCTGCTCCAGTATGCAATGCGTGGTGGTGTGCTCTC 1440
QY 1441 GTCACTTCTGCTGCTGAGGCAATCTGCTGCTGCACTTGTCAATGCTGCACTTCACT 1500
DB 1441 GTCACTTCTGCTGCTGAGGCAATCTGCTGCTGCACTTGTCAATGCTGCACTTCACT 1500
QY 1501 TACACATTCGGCAAGTACAGGGCAACAGGATCTCTACTGAAAGCGGACGCTTACCGC 1560
DB 1501 TACACATTCGGCAAGTACAGGGCAACAGGATCTCTACTGAAAGCGGACGCTTACCGC 1560
QY 1561 CTCATCCGGGAATTCACCTTCCGCGCGCTGAGCCGCTTATGCTATCTCCAC 1620
DB 1561 CTCATCCGGGAATTCACCTTCCGCGCGCTGAGCCGCTTATGCTATCTCCAC 1620
QY 1621 TTGGGCTCTGCTGCTGAGGCAATTTGCAAGGCGACCGGAGGCCCGGCTCTCCCG 1680
DB 1621 TTGGGCTCTGCTGCTGAGGCAATTTGCAAGGCGACCGGAGGCCCGGCTCTCCCG 1680
QY 1681 GCCCTGAGCAATTCGCGGTTTACCTTTCTAAGAAAGCCGAGCGGAAGCTGATACGTGG 1740
DB 1681 GCCCTGAGCAATTCGCGGTTTACCTTTCTAAGAAAGCCGAGCGGAAGCTGATACGTGG 1740
QY 1741 GAAATCGGTGATGAAGAACTTTCTGCTGGAACGCGCTAAGGACAAAGCGGAGAGCGAC 1800
DB 1741 GAAATCGGTGATGAAGAACTTTCTGCTGGAACGCGCTAAGGACAAAGCGGAGAGCGAC 1800
QY 1801 TCCGAGGCTGGAAGCGCACTGCCAGAAAGTGAATTTGGCACTGAAACAGCTGGGAC 1860
DB 1801 TCCGAGGCTGGAAGCGCACTGCCAGAAAGTGAATTTGGCACTGAAACAGCTGGGAC 1860
QY 1861 ATCCGAGATGACAAACAGCGCTGAAAGTCTGGAAGCGGAGGCTCCAGAGTGAACCTCG 1920
DB 1861 ATCCGAGATGACAAACAGCGCTGAAAGTCTGGAAGCGGAGGCTCCAGAGTGAACCTCG 1920
QY 1921 GCCCGGCACTGATGAGCTTGTCTTGAAGTGAAGCCCATGTCATCTGGGCACTGTC 1980
DB 1921 GCCCGGCACTGATGAGCTTGTCTTGAAGTGAAGCCCATGTCATCTGGGCACTGTC 1980
QY 1981 AGGACCACTTTTGGAGTGTCACTTAAACAACAAGCATGCGGCTCTCCCAAGAC 2040
DB 1981 AGGACCACTTTTGGAGTGTCACTTAAACAACAAGCATGCGGCTCTCCCAAGAC 2040
QY 2041 CAGTCCAGGCTGGAGATCAAGGCTGATCCRGAGCGTTATCCATCTGAGAGCTGC 2100
DB 2041 CAGTCCAGGCTGGAGATCAAGGCTGATCCRGAGCGTTATCCATCTGAGAGCTGC 2100